

Hale, Mary

10/27 01

From: Ulm, John
Sent: Wednesday, October 22, 2003 3:36 PM
To: Hale, Mary
Subject: RE: problem with search request for SN 09/851,494

OK, let's modify the search. I need a search of nucleotides 5500 to 7000 and 9000 to 9200 of SEQ ID NO:1, which contain specifically claimed diagnostic mutations outside of a coding region, as well as nucleotides 400 to 1500 of SEQ ID NO:2, which appears to be a coding region within SEQ ID NO:1 and which contains seven additional diagnostic mutations. If this presents a problem, I can divide SEQ ID NO:2 into fragments containing the specifically recited mutations.

-----Original Message-----

From: Hale, Mary
Sent: Tuesday, October 21, 2003 3:46 PM
To: Ulm, John
Cc: Martinell, James
Subject: RE: problem with search request for SN 09/851,494
Importance: High

per attached note

Ullah
10/22/03

~~cancel~~
~~ixm contacted 10/21~~

0101

00121 77

10/22/03
Ullah

LB
1-13,270 not
3-580 an

→ per attached note
per ixm

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2003, 18:04:00 ; Search time 441 Seconds
(without alignments)

220.243 Million cell updates/sec

Title: US-09-851-494B-3

Perfect score: 3067

Sequence: 1 MTAPAGPRGSETERLTLPNP.....CSLLCCGCRDPSEHSILVN 580

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3067	100.0	580	9	US-09-828-466-2
2	3067	100.0	580	10	US-09-965-529-13
3	3067	100.0	580	11	US-09-965-529-13
4	3067	100.0	580	14	US-10-103-458-2
5	2665	86.9	511	9	US-09-820-893-63
6	1376	44.9	538	12	US-10-114-153-26
7	1368	44.6	566	12	US-10-114-153-28
8	1367	44.6	544	12	US-10-114-153-24
9	1314	42.0	540	12	US-10-114-153-22
10	1326	40.0	255	11	US-09-866-050A-713
11	689	22.5	193	11	US-09-796-753-162
12	281.5	9.2	69	9	US-09-864-761-45089
13	152.5	5.0	621	14	US-10-005-211-2
14	152.5	5.0	966	9	US-09-828-466-6
15	150.5	4.9	76	9	US-09-864-761-41295

16	141.5	4.6	224	9	US-09-864-761-48727	Sequence 48727, A
17	139.5	4.5	179	12	US-10-029-386-32155	Sequence 32155, A
18	138	4.5	866	9	US-09-753-008-1	Sequence 1, Appli
19	127	4.1	53	9	US-09-864-761-44673	Sequence 44673, A
20	127	4.1	968	9	US-09-753-008-7	Sequence 7, Appli
21	123	4.0	724	10	US-09-796-7208-5	Sequence 5, Appli
22	123	4.0	724	12	US-10-146-733-25	Sequence 25, Appli
23	113	3.7	49	9	US-09-864-761-44699	Sequence 44699, A
24	106.5	3.5	1447	10	US-09-808-571A-2	Sequence 2, Appli
25	101	3.3	323	15	US-10-288-160-12	Sequence 12, Appli
26	100	3.3	686	12	US-10-139-572-524	Sequence 524, App
27	100	3.3	686	12	US-10-187-749-524	Sequence 524, App
28	100	3.3	686	12	US-10-194-457-524	Sequence 524, App
29	100	3.3	686	12	US-10-184-642-524	Sequence 524, App
30	100	3.3	686	12	US-10-196-747-524	Sequence 524, App
31	100	3.3	686	12	US-10-173-689-524	Sequence 524, App
32	100	3.3	686	12	US-10-173-690-524	Sequence 524, App
33	100	3.3	686	12	US-10-173-891-524	Sequence 524, App
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35	100	3.3	686	12	US-10-173-694-524	Sequence 524, App
36	100	3.3	686	12	US-10-173-698-524	Sequence 524, App
37	100	3.3	686	12	US-10-173-699-524	Sequence 524, App
38	100	3.3	686	12	US-10-173-707-524	Sequence 524, App
39	100	3.3	686	12	US-10-174-569-524	Sequence 524, App
40	100	3.3	686	12	US-10-174-583-524	Sequence 524, App
41	100	3.3	686	12	US-10-174-587-524	Sequence 524, App
42	100	3.3	686	12	US-10-174-589-524	Sequence 524, App
43	100	3.3	686	12	US-10-174-591-524	Sequence 524, App
44	100	3.3	686	12	US-10-175-736-524	Sequence 524, App
45	100	3.3	686	12	US-10-175-742-524	Sequence 524, App

ALIGNMENTS

RESULT 1

US-09-828-466-2
; Sequence 2, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Cirtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125CP
; CURRENT APPLICATION NUMBER: US/09/828,466
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/544,797
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-466-2

Query Match	100.0%;	Score 3067;	DB 9;	Length 580;
Best Local Similarity	100.0%;	Pred. No. 2.4e-289;		
Matches 580;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTAPAGPRGSETERLTLPNGYGTGAGSPAPPTPEEDLRRLKYPFMSPCDKFRAGK	60	
Db	1	MTAPAGPRGSETERLTLPNGYGTGAGSPAPPTPEEDLRRLKYPFMSPCDKFRAGK	60	
QY	61	RKPKMLQVWILVVTQILFGLSNQAVTFRRENTIAFRHLFLLYSGADDTFAAY	120	
Db	61	RKPKMLQVWILVVTQILFGLSNQAVTFRRENTIAFRHLFLLYSGADDTFAAY	120	
QY	121	TREQLYQALFHAVDQYALPDVSLGRYAVRGSGDPWTNGSLALCORYVHGHVDPAND	180	
Db	121	TREQLYQALFHAVDQYALPDVSLGRYAVRGSGDPWTNGSLALCORYVHGHVDPAND	180	
QY	181	TFDIDPMVWTDICIQDPPRPPTPPPSDDLTLLLESSSYKNLTLPKFKLVNVTIHFRLKTI	240	

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Db      181  TFDIDPMWVTDICIQVDPPEPPPPDDLTLLSSSSYKNTLKFHKLWNVTIHFRLKTI 240
Qy      241  NQSLINNEIPDCYTFVSVLITFDNKAHSGRIPISETQAHIOECKHPSVFQHGDSFRLL 300
Db      241  NQSLINNEIPDCYTFVSVLITFDNKAHSGRIPISETQAHIOECKHPSVFQHGDSFRLL 300
Qy      301  FDVVILTCSSFLCARSLLRGFLLONEFVGFMRQRGRVISLWLERLEFVNGWVILLVT 360
Db      301  FDVVILTCSSFLCARSLLRGFLLONEFVGFMRQRGRVISLWLERLEFVNGWVILLVT 360
Qy      361  SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWGVIRYLTFFHNNIILATLRV 420
Db      361  SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWGVIRYLTFFHNNIILATLRV 420
Qy      421  ALPSWMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLMSVSECLFSLINGDDMFVTFAM 480
Db      421  ALPSWMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLMSVSECLFSLINGDDMFVTFAM 480
Qy      481  QAQGRSSLVWLFSQLYLSFISLFIYMWLSLFIALTIGAYDTIKHPCGAGAESELOAY 540
Db      481  QAQGRSSLVWLFSQLYLSFISLFIYMWLSLFIALTIGAYDTIKHPCGAGAESELOAY 540
Qy      541  IAQCDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 580
Db      541  IAQCDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 580

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RESULT 2

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US-09-965-529-13
; Sequence 13, Application US/0996529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Valda
; APPLICANT: BAUGHN, Marian R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/965,529
; PRIOR FILING DATE: 2001-08-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 977658CDI
US-09-965-529-13

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Query Match      100.0%; Score 3067; DB 10; Length 580;
Best Local Similarity 100.0%; Pred. No. 2.4e-289;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MTAPAGRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
Db      1  MTAPAGRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
Qy      61  RPKCKMLQVVKILVVTQVLLFGLSNQLAVTFRENTIAFRHLFLIGYSGADDTFAAY 120
Db      61  RPKCKMLQVVKILVVTQVLLFGLSNQLAVTFRENTIAFRHLFLIGYSGADDTFAAY 120
Qy      121  TREOLYQAIHFAVDQYIALPDVSLGRYAYVRGGDPMTNGSLALCORYYHRGHVDPAND 180

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Db      121  TREOLYQAIHFAVDQYIALPDVSLGRYAYVRGGDPMTNGSLALCORYYHRGHVDPAND 180
Qy      181  TFDIDPMWVTDICIQVDPPEPPPPDDLTLLSSSSYKNTLKFHKLWNVTIHFRLKTI 240
Db      181  TFDIDPMWVTDICIQVDPPEPPPPDDLTLLSSSSYKNTLKFHKLWNVTIHFRLKTI 240
Qy      241  NQSLINNEIPDCYTFVSVLITFDNKAHSGRIPISETQAHIOECKHPSVFQHGDSFRLL 300
Db      241  NQSLINNEIPDCYTFVSVLITFDNKAHSGRIPISETQAHIOECKHPSVFQHGDSFRLL 300
Qy      301  FDVVILTCSSFLCARSLLRGFLLONEFVGFMRQRGRVISLWLERLEFVNGWVILLVT 360
Db      301  FDVVILTCSSFLCARSLLRGFLLONEFVGFMRQRGRVISLWLERLEFVNGWVILLVT 360
Qy      361  SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWGVIRYLTFFHNNIILATLRV 420
Db      361  SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWGVIRYLTFFHNNIILATLRV 420
Qy      421  ALPSWMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLMSVSECLFSLINGDDMFVTFAM 480
Db      421  ALPSWMRFCCCVAVIYLGFCGWIIVLGPYHVKFRSLMSVSECLFSLINGDDMFVTFAM 480
Qy      481  QAQGRSSLVWLFSQLYLSFISLFIYMWLSLFIALTIGAYDTIKHPCGAGAESELOAY 540
Db      481  QAQGRSSLVWLFSQLYLSFISLFIYMWLSLFIALTIGAYDTIKHPCGAGAESELOAY 540
Qy      541  IAQCDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 580
Db      541  IAQCDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 580

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RESULT 3

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US-09-969-680A-13
; Sequence 13, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BURFORD, Neil; AZIMZAI, Valda
; APPLICANT: BAUGHN, Marian R.; LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 977658CDI
US-09-969-680A-13

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Query Match      100.0%; Score 3067; DB 11; Length 580;
Best Local Similarity 100.0%; Pred. No. 2.4e-289;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MTAPAGRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
Db      1  MTAPAGRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
Qy      61  RPKCKMLQVVKILVVTQVLLFGLSNQLAVTFRENTIAFRHLFLIGYSGADDTFAAY 120
Db      61  RPKCKMLQVVKILVVTQVLLFGLSNQLAVTFRENTIAFRHLFLIGYSGADDTFAAY 120

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QY 121 TREOLYQAI PHAVDOYLALPDVSLGRVAYVRGGDPWTNGSLALCORVYHRGHVDPAND 180
 Db 121 TREOLYQAI PHAVDOYLALPDVSLGRVAYVRGGDPWTNGSLALCORVYHRGHVDPAND 180
 QY 181 TFDIDPMVVTDCIQVDPPEPPPPSDDLTLLESSSSYKNLTLPFKLVNVTIHFRLKTI 240
 Db 181 TFDIDPMVVTDCIQVDPPEPPPPSDDLTLLESSSSYKNLTLPFKLVNVTIHFRLKTI 240
 QY 241 NLOSLINNEIPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFRL 300
 Db 241 NLOSLINNEIPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFRL 300
 QY 301 FDVVVILTCSLFLLCARSLLRGLLQNEFVGFWRGRVVISLWERLEFVNGWYILLVT 360
 Db 301 FDVVVILTCSLFLLCARSLLRGLLQNEFVGFWRGRVVISLWERLEFVNGWYILLVT 360
 QY 361 SDVLTISGTMKIGIEAKNLASYDVCISLLGTSTLLVWVGIRYLTTFHNNILIALTRV 420
 Db 361 SDVLTISGTMKIGIEAKNLASYDVCISLLGTSTLLVWVGIRYLTTFHNNILIALTRV 420
 QY 421 ALPSVMRFCCCVAVIYLGFCGWI VLGPHYHVKFRSLSMVSECLFSLINGDDMFVTFPAA 480
 Db 421 ALPSVMRFCCCVAVIYLGFCGWI VLGPHYHVKFRSLSMVSECLFSLINGDDMFVTFPAA 480
 QY 481 QAOGRSSLVWLPFSOLYLYSFISLYMWLSLFTALITGAYDTIKHPGGAGABESELQAY 540
 Db 481 QAOGRSSLVWLPFSOLYLYSFISLYMWLSLFTALITGAYDTIKHPGGAGABESELQAY 540
 QY 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 580
 Db 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 580

RESULT 4

US-10-103-458-2
 ; Sequence 2, Application US/10103458
 ; Publication No. US20020197680A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Rory A.J.
 ; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
 ; FILE REFERENCE: NMI-125
 ; CURRENT APPLICATION NUMBER: US/10/103,458
 ; CURRENT FILING DATE: 2002-03-22
 ; PRIOR APPLICATION NUMBER: US/09/544,797
 ; PRIOR FILING DATE: PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 580
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-103-458-2

Query Match 100.0%; Score 3067; DB 14; Length 580;
 Best Local Similarity 100.0%; Pred. No. 2,4e-289;
 Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTAPAGRGSETERLITPNPGYGTQAGSPAPPTPEEEDLRRLKYFFMSPCDKFRAG 60
 Db 1 MTAPAGRGSETERLITPNPGYGTQAGSPAPPTPEEEDLRRLKYFFMSPCDKFRAG 60
 QY 61 RKPKLMLQVVKLVVTVQILFGLSNQLAVTFRRENTIAFRHLFLGLYSGDADDTFAAY 120
 Db 61 RKPKLMLQVVKLVVTVQILFGLSNQLAVTFRRENTIAFRHLFLGLYSGDADDTFAAY 120
 QY 121 TREOLYQAI PHAVDOYLALPDVSLGRVAYVRGGDPWTNGSLALCORVYHRGHVDPAND 180
 Db 121 TREOLYQAI PHAVDOYLALPDVSLGRVAYVRGGDPWTNGSLALCORVYHRGHVDPAND 180
 QY 181 TFDIDPMVVTDCIQVDPPEPPPPSDDLTLLESSSSYKNLTLPFKLVNVTIHFRLKTI 240
 Db 181 TFDIDPMVVTDCIQVDPPEPPPPSDDLTLLESSSSYKNLTLPFKLVNVTIHFRLKTI 240

QY 241 NLOSLINNEIPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFRL 300
 Db 241 NLOSLINNEIPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFRL 300
 QY 301 FDVVVILTCSLFLLCARSLLRGLLQNEFVGFWRGRVVISLWERLEFVNGWYILLVT 360
 Db 301 FDVVVILTCSLFLLCARSLLRGLLQNEFVGFWRGRVVISLWERLEFVNGWYILLVT 360
 QY 361 SDVLTISGTMKIGIEAKNLASYDVCISLLGTSTLLVWVGIRYLTTFHNNILIALTRV 420
 Db 361 SDVLTISGTMKIGIEAKNLASYDVCISLLGTSTLLVWVGIRYLTTFHNNILIALTRV 420
 QY 421 ALPSVMRFCCCVAVIYLGFCGWI VLGPHYHVKFRSLSMVSECLFSLINGDDMFVTFPAA 480
 Db 421 ALPSVMRFCCCVAVIYLGFCGWI VLGPHYHVKFRSLSMVSECLFSLINGDDMFVTFPAA 480
 QY 481 QAOGRSSLVWLPFSOLYLYSFISLYMWLSLFTALITGAYDTIKHPGGAGABESELQAY 540
 Db 481 QAOGRSSLVWLPFSOLYLYSFISLYMWLSLFTALITGAYDTIKHPGGAGABESELQAY 540
 QY 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 580
 Db 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 580

RESULT 5

US-09-820-893-63
 ; Sequence 63, Application US/09820893
 ; Patent No. US20020076705A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 31 Human Secreted Proteins
 ; FILE REFERENCE: PZ033PI
 ; CURRENT APPLICATION NUMBER: US/09/820,893
 ; CURRENT FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: 09/531,119
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: 60/102,895
 ; PRIOR FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 140
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 63
 ; LENGTH: 511
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (135)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-820-893-63

Query Match 86.9%; Score 2665; DB 9; Length 511;
 Best Local Similarity 99.2%; Pred. No. 2.5e-250;
 Matches 507; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 70 VVKILVTVQLILFGLSNQLAVTFRRENTIAFRHLFLGLYSGADDTFAAYTREQLYQAI 129
 Db 1 VVKILVTVQLILFGLSNQLAVTFRRENTIAFRHLFLGLYSGADDTFAAYTREQLYQAI 60
 QY 130 PHAVDOYLALPDVSLGRVAYVRGGDPWTNGSLALCORVYHRGHVDPANDTFDIDPMV 189
 Db 61 PHAVDOYLALPDVSLGRVAYVRGGDPWTNGSLALCORVYHRGHVDPANDTFDIDPMV 120
 QY 190 TDCIQVDPPEPPPPSDDLTLLESSSSYKNLTLPFKLVNVTIHFRLKTIINQSLINNE 249
 Db 121 TDCIQVDPPEPPPPSDDLTLLESSSSYKNLTLPFKLVNVTIHFRLKTIINQSLINNE 180
 QY 250 IPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFRLFDVVVILTC 309
 Db 181 IPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDNFRLFDVVVILTC 240
 QY 310 SLSFLLCARSLLRGLLQNEFVGFWRGRVVISLWERLEFVNGWYILLVTSDVLTISGT 369

Db 241 SLSELCARSLRGLQNEFVGFMRQRGRVLSWERLEFVNGWILLVTSVITISGT 300
Qy 370 IMKIGIEAKNLASYDVCSILLGTSTLLVWVGVRILTFFPHNYNIIATLRVALPSVMRFC 429
Db 301 IMKIGIEAKNLASYDVCSILLGTSTLLVWVGVRILTFFPHNYNIIATLRVALPSVMRFC 360
Qy 430 CCVAVILGYCFGCVILGPHVHRSLSMVSECLFSLINGDDMFVTFAMQAQGRSSL 489
Db 361 CCVAVILGYCFGCVILGPHVHRSLSMVSECLFSLINGDDMFVTFAMQAQGRSSL 420
Qy 490 VWLFSQLYLSFISFIYMWLSLFIATITGAYDTIKHPGAGAESELOQYIAQCODSPT 549
Db 421 VWLFSQLYLSFISFIYMWLSLFIATITGAYDTIKHPGAGAESELOQYIAQCODSPT 480
Qy 550 SGKFRGSGSACSLCCGRDPSSEHSLIVN 580
Db 481 SGKFRGSGARACSLCCGRDPSSEHSLIVN 511

RESULT 6

US-10-114-153-26

; Sequence 26, Application US/10114153
; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Tchernev, Velizar

; APPLICANT: Gangolli, Esha

; APPLICANT: Vernet, Corine

; APPLICANT: Spytek, Kimberly

; APPLICANT: Malyankar, Uriel

; APPLICANT: Patturajan, Meera

; APPLICANT: Miller, Charles

; APPLICANT: Taupier, Raymond J. Jr.

; APPLICANT: Hayes, Melvyn

; APPLICANT: Ju, Jingfang

; APPLICANT: Peyman, John

; APPLICANT: Catterton, Elina

; APPLICANT: MacDougall, John

; APPLICANT: Edinger, Shlomit

; APPLICANT: Stone, David

; APPLICANT: Mazur, Ann

; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI

; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE

; FILE REFERENCE: 21402-322A

; CURRENT APPLICATION NUMBER: US/10/114,153

; CURRENT FILING DATE: 2002-08-06

; PRIOR APPLICATION NUMBER: 60/281086

; PRIOR FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: 60/281906

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/282020

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/282930

; PRIOR FILING DATE: 2001-04-10

; PRIOR APPLICATION NUMBER: 60/283512

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: 60/283444

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: 60/283657

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/283710

; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 26
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-26

Query Match

44.9%; Score 1376; DB 12; Length 538;

Best Local Similarity 48.9%; Pred. No. 7.1e-125;

Matches 268; Conservative 115; Mismatches 143; Indels 22; Gaps 8;

Qy 37 EEDLRRLRYFFMSPCDKPRAGKPKCKMLQVVKILVTVQLILFGLSNQLAVTFREE 96
Db 9 KEECLREDLKFYFMSPCCKYRARRQIEPKLGLQLIKIVMTQTQVRFGLSNQLVAFKED 68
Qy 97 NTIAFRHLFLIGYSDGADDTF--AAATREQLYQAIHFAVDQYLALPDVSLGRYAVRGG 154
Db 69 NTVAFKELFLKGYSGTDEDDYSCSVYTOEAYESIFPAINQYHOLKDIITLGLY----G 124
Qy 155 DPWTNGSGLACQRYHRGHVDPANDTFIDPMVVTDCIQVDPPEPPPPSPDDLTLES 214
Db 125 ENEDNRIGLKVKCKQHYKGTMTFNSNETLNDVDELDCVQLDQLSKKPPD----WKN 179
Qy 215 SSSYKNLTLPKFKLVNVTIHFRLKTNLOSINNNEIPDCYTFSLITFDNKAHSGRIPIS 274
Db 180 SSFPR---LEFYRLQVEISFHLKGDIDQTHSRELPCYVFQNTIIFDNKAHSGKIKY 236
Qy 275 LETQAHIECKHPSVFQHGDS--FRLLFDVVVILTCSLSPLLCARSLRGLLQNEFVG 332
Db 237 FDSDAKIECKDLNIFGSAQKNAQYVLVDAFVIVICLASILLCTRISIVLRLRKRFLN 296
Qy 333 FMRQRQVRISLWERLEFVNGWILLVTSVLTISGTMKIGIEAKNLASYDVCSILLGT 392
Db 297 FFEKXKRPVCDTDQWEEFNGWYLVIIISDLMTIIGSILKWEIKAKNLTYDLCISIFLT 356
Qy 393 STLLVWVGVRILTFFPHNYNIIATLRVALPSVMRFFCCVAVIYLGFCGCVILGPHV 452
Db 357 STLLVWVGVRILGYFOAYNVNLTMOASLPKVLRFCAAGMIYLGTFCGWIVLGYHD 416
Qy 453 KFRSLMSVSECLFSLINGDDMFVTFAMQAQGRSSLVWLPFSOLYLSFISFIYMWLSL 512
Db 417 KFENLNTVAECLFSLVNGDDMFATFA--QIQQ-KSILVWLPFSRLYLSFISFIYMWLSL 473
Qy 513 FIALITQAYDTIKHPGAGAESELOQYIAQCODSPTSGKFRGSGSACSLCCGRDPS 572
Db 474 FIALITDSYDTIKKQQNGFPETDLOEFLKECS---SKEEYQKESAFSLSCICRRRKR 530
Qy 573 BEHSLIVN 580
Db 531 DDHLIPIS 538

RESULT 7

US-10-114-153-28

; Sequence 28, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

```
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Paturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC AC
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; PRIOR FILING DATE: 2002-08-06
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 28
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-28

Query Match      44.6%; Score 1368; DB 12; Length 566;
Best Local Similarity 48.7%; Fred.No. 4.6e-124;
Matches 267; Conservative 115; Mismatches 144; Indels 22; Gaps 8;

QY 37 EEDLERLKLKYPFPCDFKAGKPKMLQVVKILVTVQLTFLGSLNQLATFREE 96
DB 37 KEEDLERLKLKYPFPCDFKAGKPKMLQVVKILVTVQLTFLGSLNQLATFREE 96
QY 97 NTIAPRHLLGYSOGADTF--AAYTRQLYQAIHFAVDQVLAIPDVSLGRYAYVRGG 154
DB 97 NTIAPRHLLGYSOGADTF--AAYTRQLYQAIHFAVDQVLAIPDVSLGRYAYVRGG 154
QY 97 NTIAPRHLLGYSOGADTF--AAYTRQLYQAIHFAVDQVLAIPDVSLGRYAYVRGG 152
DB 97 NTIAPRHLLGYSOGADTF--AAYTRQLYQAIHFAVDQVLAIPDVSLGRYAYVRGG 152
QY 155 DPWTGSLGALCORYYHGRVHPDPTDIDPMVYTCIQVDPPRPPPPSDDLTLLES 214
DB 155 DPWTGSLGALCORYYHGRVHPDPTDIDPMVYTCIQVDPPRPPPPSDDLTLLES 214
QY 215 SSSYKNLTAKFKHNVNTHFLKTNINQSLINNEIPCYTFPSVLITFDNKAHSGRIPIS 274
DB 215 SSSYKNLTAKFKHNVNTHFLKTNINQSLINNEIPCYTFPSVLITFDNKAHSGRIPIS 274
QY 208 SFFR---LEFYELLQVEISFLKIDLOTIHSRLPDCYVFQNTIIFDNKAHSGKIKY 264
DB 208 SFFR---LEFYELLQVEISFLKIDLOTIHSRLPDCYVFQNTIIFDNKAHSGKIKY 264
QY 275 LSTQAHIQECKPSPVPHQDNGS--FRLPFDVVVITLCSLFLCARSLRLRFLQNEPVG 332
DB 275 LSTQAHIQECKPSPVPHQDNGS--FRLPFDVVVITLCSLFLCARSLRLRFLQNEPVG 332
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Db 265 FSDDAKIECKDNLNIFGSAQKNAQVVLVDFAFVIVICLASILCTRISIVLALRLKRELN 324
QY 333 FNRQGRVISLWERLEFVNGWYILLVTSVDLTISGTTIMKIGIEAKNLASYDVCSILLGT 392
Db 325 FFLEKYKRPVCDTDQWFEINGWYVLVLSIDMTIIGSLKWEIKAKNLNVDLCSIFLGT 384
QY 393 STLLVWVGVRVLTPTPHNYNLIATLRVALPSVMEFCCCVAVIYLGVCFCGWIIVLGPYHV 452
Db 385 STLLVWVGVRVLTPTPHNYNLIATLRVALPSVMEFCCCVAVIYLGVCFCGWIIVLGPYHV 444
QY 453 KPSLSMVSECLFSLINGDDMFVTFPAAMQAQGRSSSLVWLFSQLYLSIFSIYIWMVLSL 512
Db 445 KEENLNTVAECLFSLVNGDDMFATFA--QIQQ-KSILWLFSLYLSIFSIYIWMVLSL 501
QY 513 FIALITGAYDTIKHFGGAGABESELQAYIAQODSPTSGKFRGSGSACSLCCGCRDPS 572
Db 502 FIALITDSYDTIKFPQNGFPETDQLEFKES---SKEEYQKESAFSLCICRRRRRS 558
QY 573 BEHSLVN 580
Db 559 DDHLLPIS 566

RESULT 8
US-10-114-153-24
; Sequence 24, Application US/10114153
; Publication No. US20030185815A1.
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Paturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC AC
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2003, 17:43:58 ; Search time 90 seconds
(without alignments)

1663.006 Million cell updates/sec

Title: US-09-851-494B-3

Perfect score: 3067

Sequence: 1 MTAAPAGRGSETERLLTPNP.....CSLLCCGCRDPSEHSLN 580

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_invertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB ID	Description
1	3067	100.0	580	4 Q9GZU1	Q9GZU1 homo sapien
2	3059	99.7	580	4 Q9H4B3	Q9H4B3 homo sapien
3	2884.5	94.0	581	4 Q9H292	Q9H292 homo sapien
4	2820	91.9	580	11 Q99J21	Q99J21 mus musculus
5	1859.5	60.6	545	4 Q9H4B5	Q9H4B5 homo sapien
6	1628.5	53.1	594	11 Q9BS73	Q9BS73 mus musculus
7	1626.5	53.0	553	11 Q9R4F0	Q9R4F0 mus musculus
8	1626.5	53.0	591	11 Q9BSG1	Q9BSG1 mus musculus
9	1623.5	52.9	593	11 Q9CDB2	Q9CDB2 mus musculus
10	1621	52.9	553	4 Q9TDD5	Q9TDD5 homo sapien
11	1396	45.5	497	4 Q9NV09	Q9NV09 homo sapien
12	1374	44.8	538	4 Q8IZK6	Q8IZK6 homo sapien
13	1335	43.5	538	11 Q9CQD3	Q9CQD3 mus musculus
14	1335	43.5	566	11 Q8K595	Q8K595 mus musculus
15	1332	43.4	538	11 Q8K2T6	Q8K2T6 mus musculus
16	1025.5	33.4	652	5 Q9VW35	Q9VW35 drosophila

17	783	25.5	609	5 Q8T877	Q8T877 caenorhabdi
18	783	25.5	666	5 Q8T878	Q8T878 caenorhabdi
19	777	25.3	611	5 Q8J556	Q8J556 caenorhabdi
20	777	25.3	668	5 Q8T666	Q8T666 caenorhabdi
21	776	25.3	644	5 Q8WSP3	Q8WSP3 caenorhabdi
22	385	12.6	175	4 Q8N9R3	Q8N9R3 homo sapien
23	161.5	5.3	897	5 Q9VK95	Q9VK95 drosophila
24	151.5	4.9	966	11 Q8BPR6	Q8BPR6 mus musculus
25	139.5	4.5	660	13 Q8AW53	Q8AW53 brachydanio
26	127.5	4.2	199	11 Q8C029	Q8C029 mus musculus
27	125	4.1	733	10 Q948T1	Q948T1 arabidopsis
28	124	4.0	665	4 Q9S814	Q9S814 homo sapien
29	123	4.0	724	10 Q9ZT83	Q9ZT83 arabidopsis
30	123	4.0	733	10 Q94K18	Q94K18 arabidopsis
31	115.5	3.8	1274	5 Q9VSO9	Q9VSO9 drosophila
32	115	3.7	420	8 Q8HN35	Q8HN35 paragonimus
33	115	3.7	482	12 Q81013	Q81013 herpesvirus
34	111.5	3.6	775	5 Q9ULS7	Q9ULS7 caenorhabdi
35	111.5	3.6	2300	5 Q8IP23	Q8IP23 drosophila
36	111.5	3.6	2516	5 Q9V3P7	Q9V3P7 drosophila
37	111.5	3.6	2519	5 Q8IP25	Q8IP25 drosophila
38	111.5	3.6	2552	5 Q8IP24	Q8IP24 drosophila
39	111	3.6	321	16 Q8CNG5	Q8CNG5 staphylococ
40	111	3.6	400	16 Q9TER0	Q9TER0 clostridium
41	110.5	3.6	310	8 P92079	P92079 menosoma ci
42	109	3.6	420	8 Q9MLH8	Q9MLH8 paragonimus
43	109	3.6	793	3 Q08967	Q08967 saccharomyc
44	108.5	3.5	2196	5 P91744	P91744 loligo blue
45	108	3.5	2221	5 Q9NKKV1	Q9NKKV1 halocynthia

ALIGNMENTS

RESULT 1

Q9GZU1	Q9GZU1	PRELIMINARY;	PRT;	580 AA.
ID	Q9GZU1	PRELIMINARY;	PRT;	580 AA.
AC	Q9GZU1	Q9GZU1		
DT	01-MAR-2001	(TRENBLrel. 16, Created)		
DT	01-MAR-2001	(TRENBLrel. 16, Last sequence update)		
DE	01-MAR-2003	(TRENBLrel. 23, Last annotation update)		
DE	Hypothetical protein FLJ22449 (Mucolipin) (Mucolipidosis type IV			
DE	protein) (Mucolipin 1).			
GN	MCOLN1 OR MLIV.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA	Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,			
RA	Tanaka T., Nakamura Y., Isogai T., Sugano S.;			
RT	"MEDO human CDNA sequencing project."			
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA	Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,			
RA	Tanaka T., Nakamura Y., Isogai T., Sugano S.;			
RT	"MEDO human CDNA sequencing project."			
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=20485419; PubMed=11030752;			
RA	Sun M., Goldin E., Stahl S., Falardeau J.L., Kennedy J.C.,			
RA	Acterno J.S. Jr., Bove C., Kaneshi C.R., Nagle J., Bromley M.C.,			
RA	Colman M., Schiffrin R., Slaughter S.A.;			
RT	"Mucolipidosis type IV is caused by mutations in a gene encoding a			
RT	novel transient receptor potential channel."			
RL	Hum. Mol. Genet. 9:2471-2478(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=20428196; PubMed=10973263;			
RA	Bargal R., Avidan N., Ben-Asher E., Olender Z., Zeigler M.,			
RA	Frumkin A., Raas-Rothschild A., Glusman G., Lancet D., Bach G.;			
RT	"Identification of the gene causing mucopolipidosis type IV."			
RL	Nat. Genet. 26:118-121(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			

RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK026102; BAB15360.1; -
 DR EMBL; AF287269; AAG00797.1; -
 DR EMBL; AF287270; AAG00798.1; -
 DR EMBL; AF249319; AAG10422.1; -
 DR EMBL; BC005149; AHA05149.1; -
 DR Genew; HGNC:13356; MCOLN1.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000734; Lipase.
 DR Pfam; PF00520; Ion_trans; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 DR Hypothetical protein; Ionic channel; Transmembrane.
 KW Hypothetical protein; Ionic channel; Transmembrane.
 SQ SEQUENCE 580 AA; 65022 MW; 7E7691F58D01C804 CRC64;

Query Match 100.0%; Score 3067; DB 4; Length 580;
 Best Local Similarity 100.0%; Pred. No. 5.9e-265; Indels 0; Gaps 0;
 Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPAGPRGSTERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
 DB 1 MTPAGPRGSTERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
 QY 61 RKPKMLQVVKILVVTQVLLFGLSNQLAVTFRENTIAFRHLFLLYSGDADDTFAA 120
 DB 61 RKPKMLQVVKILVVTQVLLFGLSNQLAVTFRENTIAFRHLFLLYSGDADDTFAA 120
 QY 121 TREQLYQAIHFAVDQYALPDVSLGRYAYVRGGDPMTNGSLGALCORYYHRGHVDPA 180
 DB 121 TREQLYQAIHFAVDQYALPDVSLGRYAYVRGGDPMTNGSLGALCORYYHRGHVDPA 180
 QY 181 TFDIDPMVVTDCIQVDPPERPPPPDDLTLLSSSSYKNLTLPKHLVNVTHFRUKTI 240
 DB 181 TFDIDPMVVTDCIQVDPPERPPPPDDLTLLSSSSYKNLTLPKHLVNVTHFRUKTI 240
 QY 241 NLOSLINNEIPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDSRLL 300
 DB 241 NLOSLINNEIPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDSRLL 300
 QY 301 FDVVVILTCSLFLLCARSLRGFLQNEFVGFWMRQGRVISLWERLEFVNGWYILLVT 360
 DB 301 FDVVVILTCSLFLLCARSLRGFLQNEFVGFWMRQGRVISLWERLEFVNGWYILLVT 360
 QY 361 SDVLTISGTMKIGIEAKNLASYDVCISLLGTSTLLVWVGVIYRILTFPHNYNLIATLRV 420
 DB 361 SDVLTISGTMKIGIEAKNLASYDVCISLLGTSTLLVWVGVIYRILTFPHNYNLIATLRV 420
 QY 421 ALPSVMRFCCCAVIVLYGFCGWIIVLGPVHKFRSLSMVSECLFSLINGDDMPVTFAM 480
 DB 421 ALPSVMRFCCCAVIVLYGFCGWIIVLGPVHKFRSLSMVSECLFSLINGDDMPVTFAM 480
 QY 481 QAOQGRSSLVWLFSQLYLSFISLFIYVWLSLFIALITGAYDTIKHPGGAGASELOAY 540
 DB 481 QAOQGRSSLVWLFSQLYLSFISLFIYVWLSLFIALITGAYDTIKHPGGAGASELOAY 540
 QY 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLLVN 580
 DB 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLLVN 580

RESULT 2
 Q9H4B3 PRELIMINARY; PRT; 580 AA.
 ID Q9H4B3;
 AC Q9H4B3;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Mucolipidin.
 GN M4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 (1)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20489855; PubMed=1103137;
 RX Bassi M.T.; Manzoni M.; Monti E.; Pizzo M.T.; Ballabio A.; Borsani G.;
 RA "Cloning of the gene encoding a novel integral membrane protein,
 RT mucolipidin, and identification of the two major founder mutations
 RT causing mucopolipidosis type IV";
 RL Am. J. Hum. Genet. 67:1110-1120(2000).
 DR EMBL; AJ293970; CAC08215.1; -
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000734; Lipase.
 DR Pfam; PF00520; Ion_trans; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Ionic channel; Transmembrane.
 SQ SEQUENCE 580 AA; 65012 MW; 6CEB53645D010705 CRC64;

Query Match 99.7%; Score 3059; DB 4; Length 580;
 Best Local Similarity 99.8%; Pred. No. 3.1e-264; Indels 0; Gaps 0;
 Matches 579; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTPAGPRGSTERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
 DB 1 MTPAGPRGSTERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
 QY 61 RKPKMLQVVKILVVTQVLLFGLSNQLAVTFRENTIAFRHLFLLYSGDADDTFAA 120
 DB 61 RKPKMLQVVKILVVTQVLLFGLSNQLAVTFRENTIAFRHLFLLYSGDADDTFAA 120
 QY 121 TREQLYQAIHFAVDQYALPDVSLGRYAYVRGGDPMTNGSLGALCORYYHRGHVDPA 180
 DB 121 TREQLYQAIHFAVDQYALPDVSLGRYAYVRGGDPMTNGSLGALCORYYHRGHVDPA 180
 QY 181 TFDIDPMVVTDCIQVDPPERPPPPDDLTLLSSSSYKNLTLPKHLVNVTHFRUKTI 240
 DB 181 TFDIDPMVVTDCIQVDPPERPPPPDDLTLLSSSSYKNLTLPKHLVNVTHFRUKTI 240
 QY 241 NLOSLINNEIPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDSRLL 300
 DB 241 NLOSLINNEIPDCYTFVSLITFDNKAHSGRIPISLETQAHIOECKHPSVFQHGDSRLL 300
 QY 301 FDVVVILTCSLFLLCARSLRGFLQNEFVGFWMRQGRVISLWERLEFVNGWYILLVT 360
 DB 301 FDVVVILTCSLFLLCARSLRGFLQNEFVGFWMRQGRVISLWERLEFVNGWYILLVT 360
 QY 361 SDVLTISGTMKIGIEAKNLASYDVCISLLGTSTLLVWVGVIYRILTFPHNYNLIATLRV 420
 DB 361 SDVLTISGTMKIGIEAKNLASYDVCISLLGTSTLLVWVGVIYRILTFPHNYNLIATLRV 420
 QY 421 ALPSVMRFCCCAVIVLYGFCGWIIVLGPVHKFRSLSMVSECLFSLINGDDMPVTFAM 480
 DB 421 ALPSVMRFCCCAVIVLYGFCGWIIVLGPVHKFRSLSMVSECLFSLINGDDMPVTFAM 480
 QY 481 QAOQGRSSLVWLFSQLYLSFISLFIYVWLSLFIALITGAYDTIKHPGGAGASELOAY 540
 DB 481 QAOQGRSSLVWLFSQLYLSFISLFIYVWLSLFIALITGAYDTIKHPGGAGASELOAY 540
 QY 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLLVN 580
 DB 541 IAQCQDSPTSGKFRGSGSACSLCCCGRDPSEHSLLVN 580

RESULT 3
 Q9H292 PRELIMINARY; PRT; 581 AA.
 ID Q9H292;
 AC Q9H292;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Mucolipin 1.
 GN MCOLN1.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20428196; PubMed=10973263;
RA Bargal R., Avidan N., Ben-Asher E., Olender Z., Zeigler M.,
RA Frumkin A., Raas-Rothschild A., Glusman G., Lancet D., Bach G.;
RT "Identification of the gene causing mucopolipidosis type IV.";
RL Nat. Genet. 26:118-123(2000).
DR EMBL; AF305575; AAC42242.1; JOINED.
DR EMBL; AF305576; AAC42242.1; JOINED.
DR EMBL; AF305577; AAC42242.1; JOINED.
DR EMBL; AF305578; AAC42242.1; JOINED.
DR EMBL; AF305579; AAC42242.1; JOINED.
DR EMBL; AF305576; AAC42242.1; JOINED.
DR EMBL; AF305577; AAC42242.1; JOINED.
DR EMBL; AF305578; AAC42242.1; JOINED.
DR EMBL; AF305579; AAC42242.1; JOINED.
DR InterPro; IPR005821; Cat channel_TripL.
DR InterPro; IPR005821; Cat channel_TripL.
DR Pfam; PF00520; ion_trans.1.
DR PROSITE; PS00120; LIPASE_SER.1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 581 AA; 65099 MW; 342B4B558C891112 CRC64;

Query Match 94.0%; Score 2884.5; DB 4; Length 581;
Best Local Similarity 94.9%; Pred. No. 1.le-248;
Matches 555; Conservative 5; Mismatches 16; Indels 9; Gaps 2;

QY 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
DB 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
QY 61 RPKCKLMQVVKLVVTVQLILFGLSNQLAVTFRRENTIAFRHLFLGYSDGADDTFAAY 120
DB 61 RPKCKLMQVVKLVVTVQLILFGLSNQLAVTFRRENTIAFRHLFLGYSDGADDTFAAY 120
QY 121 TREQLYQALFHAVDOYLALPDVSLGRYAYVRGGDPWTNGSL-----ALCQRYHGRHV 175
DB 121 TREQLYQALFHAVDOYLALPDVSLGRYAYVRGGDPWTNGSL-----ALCQRYHGRHV 175
QY 176 DPANDTFDDPMVVTDCIQVDPERPPPPSDDTLTLESSSYKNLTLPKHLVNTIHF 235
DB 176 -PITHLTLRWLLVNCIQVDPERPPPPSDDTLTLESSSYKNLTLPKHLVNTIHF 235
QY 236 RLKTNLQSLINNEIPDCYTFSSVLTITFDNKAHSGRIPISLETQAHIQECKHPSVFOHGDN 295
DB 237 RLKTNLQSLINNEIPDCYTFSSVLTITFDNKAHSGRIPISLETQAHIQECKHPSVFOHGDN 295
QY 296 SPRLFLPDVVVITCSLUSFLCARSLRGFLQNEFVGFPMWRQGRVVISLWERLEFVNGWY 355
DB 297 SPRLFLPDVVVITCSLUSFLCARSLRGFLQNEFVGFPMWRQGRVVISLWERLEFVNGWY 355
QY 356 ILLVTSDDLVTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFPHNINILI 415
DB 357 ILLVTSDDLVTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGVIYRLTFPHNINILI 415
QY 416 ATRVALPSWMPFCCCVAVIYLGFCGVIPLGPHYKFRSLSMVSECLFSLINGDDMEV 475
DB 417 ATRVALPSWMPFCCCVAVIYLGFCGVIPLGPHYKFRSLSMVSECLFSLINGDDMEV 475
QY 476 TFAAQAQGRSLWFLFQSLYLSIFLFIYVLSLFIATLTGAVDTTIKHPGGAES 535
DB 477 TFAAQAQGRSLWFLFQSLYLSIFLFIYVLSLFIATLTGAVDTTIKHPGGAES 535
QY 536 ELQAVIAQCDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 580
DB 537 ELQAVIAQCDSPTSGKFRGSGSACSLCCCGRDPSEHSLVN 581

Query Match 91.9%; Score 2820; DB 11; Length 580;
Best Local Similarity 91.4%; Pred. No. 6.5e-243;
Matches 530; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
DB 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRRLKYFFMSPCDKFRAG 60
QY 61 RPKCKLMQVVKLVVTVQLILFGLSNQLAVTFRRENTIAFRHLFLGYSDGADDTFAAY 120
DB 61 RPKCKLMQVVKLVVTVQLILFGLSNQLAVTFRRENTIAFRHLFLGYSDGADDTFAAY 120
QY 121 TREQLYQALFHAVDOYLALPDVSLGRYAYVRGGDPWTNGSLALCORYHGRHVDPAND 180
DB 121 TOEQYQALFHAVDOYLALPDVSLGRYAYVRGGDPWTNGSLALCORYHGRHVDPAND 180
QY 181 TFDIDPMVVTDCIQVDPERPPPPSDDTLTLESSSYKNLTLPKHLVNTIHFRLKTI 240
DB 181 TFDIDPMVVTDCIQVDPERPPPPSDDTLTLESSSYKNLTLPKHLVNTIHFRLKTI 240
QY 241 NLQSLINNEIPDCYTFSSVLTITFDNKAHSGRIPISLETQAHIQECKHPSVFOHGDNSFRLL 300
DB 241 NLQSLINNEIPDCYTFSSVLTITFDNKAHSGRIPISLETQAHIQECKHPSVFOHGDNSFRLL 300
QY 301 FQVVTLCSTLUSFLCARSLRGFLQNEFVGFPMWRQGRVVISLWERLEFVNGWYILLVT 360

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Db 301 FDVVVILTCSLFLLCARSLRGLQLQNEFVVMRRRRGREISLWERLEFVNGVILLVT 360
QY 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGIRYLTFFHNYNLIATLRV 420
Db 361 SDVLTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGIRYLTFFHNYNLIATLRV 420
QY 421 ALPSVMRFCCCVAVIYLVGFCGWTVLGPHYHVKFSLSMVSECLFSLINGDDMFVTFAM 480
Db 421 ALPSVMRFCCCVAVIYLVGFCGWTVLGPHYHVKFSLSMVSECLFSLINGDDMFVTFAM 480
QY 481 QAQGRSSVLWFLFSLYLSFISFIYVWLSFIALITGAYDTIKHPGGAGAESELOAY 540
Db 481 QAQGRSSVLWFLFSLYLSFISFIYVWLSFIALITGAYDTIKHPGGAGAESELOAY 540
QY 541 IAQODSPTSGKFRGSGASLCCCGRDPSEHSLLVN 580
Db 541 IEQCQDSPTSGKFRGSGASLFCGCCGRDPSEHSLLVN 580

RESULT 5
Q9H4B5 PRELIMINARY; PRT; 545 AA.
AC Q9H4B5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
DE Mucolipidin.
GN M4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20489855; PubMed=11013137;
RT "Cloning of the gene encoding a novel integral membrane protein,
RT mucolipidin, and identification of the two major founder mutations
RT causing mucopolipidosis type IV.";
RL Am. J. Hum. Genet. 67:1110-1120(2000).
DR EMBL; AJ293659; CAC07813.1; -
DR InterPro; IPR002111; Cat channel_Trlp.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; ion_trans; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 545 AA; 60608 MW; 55179F72029D65C3 CRC64;

Query Match 60.6%; Score 1859.5; DB 4; Length 545;
Best Local Similarity 93.8%; Pred. No. 3e-157;
Matches 360; Conservative 2; Mismatches 5; Indels 17; Gaps 2;

QY 197 PPERPPPPDDLTLLSSSSYKNTLKFHKLNVNTHFRLKTNLQSLINNEIPDCYTF 256
Db 179 PEDAPDPPS-----LLP-----RLNVNTHFRLKTNLQSLINNEIPDCYTF 221
QY 257 SVLITFDNKAHSGRIPISLETQAHIQCKHPSVFOHGDNSFRLLFDVVILTCSLSPLLC 316
Db 222 SVLITFDNKAHSGRIPISLETQAHIQCKHPSVFOHGDNSFRLLFDVVILTCSLSPLLC 281
QY 317 ARSLRGLFLQNEFVGMFWRQGRVLSLWERLEFVNGVILLVTSVLTSGTIMKIGIE 376
Db 282 ARSLRGLFLQNEFVGMFWRQGRVLSLWERLEFVNGVILLVTSVLTSGTIMKIGIE 341
QY 377 AKNLASVDVCSILLGTSTLLVWVGIRYLTFFHNYNLIATLRVALPSVMRFCCCVAVIY 436
Db 342 AKNLASVDVCSILLGTSTLLVWVGIRYLTFFHNYNLIATLRVALPSVMRFCCCVAVIY 401
QY 437 LGVCFPCGWIYLVGPHYHVKFSLSMVSECLFSLINGDDMFVTFAMQAQGRSSVLWFLFSQL 496
Db 402 LGVCFPCGWIYLVGPHYHVKFSLSMVSECLFSLINGDDMFVTFAMQAQGRSSVLWFLFSQL 461
QY 497 YLYSFSISLFIYVWLSFIALITGAYDTIKHPGGAGAESELOAYIAQODSPTSGKFRG 556

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Db 462 YLYSFSISLFIYVWLSFIALITGAYDTIKHPGGAGAESELOAYIAQODSPTSGKFRG 521
QY 557 SGSACSLILCCGRDPSEHSLLVN 580
Db 522 SGSACSLILCCGRDPSEHSLLVN 545

RESULT 6
Q8BS73 PRELIMINARY; PRT; 594 AA.
AC Q8BS73;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE Weakly similar to MUCOLIPIDIN (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK035029; BAC28916.1; -
DR NON TER
FT
SQ SEQUENCE 594 AA; 68259 MW; 958DA443C786E45C CRC64;

Query Match 53.1%; Score 1628.5; DB 11; Length 594;
Best Local Similarity 55.5%; Pred. No. 1.4e-136;
Matches 313; Conservative 91; Mismatches 121; Indels 39; Gaps 6;

QY 7 PROSETERLLTPNPGVGTQAGSPAPPTPEEEDLRRLKYFPMSPCKDPRAKGRKPKL 66
Db 65 PSSSPSEQLL-----EQMRKLFKFFFMNPKETWARGKPKWL 104
QY 67 MLOVVKILVVTVOLILFGLSNQLAVTFRENTIAFHLFLLGYSGDADDTFAATREQLY 126
Db 105 AIQILKIAMVTIQLVLFGLSNQMVAVKENTIAFKHLFLKGYMDRMDDTYAVYTQSEVY 164
QY 127 QAIFHAVDQYALDPLDVSIGRYAVYVGGDPWTNGSLGLCORVYHGHVDPANDTIDIP 186
Db 165 DQIIFAVTQYLOLONISVGNHAYENK-----TKQSMAICQHFYRGTTCPGNDITDIDP 220
QY 187 MVVTDICQVDPPPPPPPSDDLTLLESSSYK-NLTLPFKLVNVTIHFRLKTNLQSL 245
Db 221 EVETECFLVEP-----DEASHLGTGPKGNKLNLSLDFHRLTLVELQFKLXAINLQTV 271
QY 246 INNEIPDCYTFESVLTIFDNKAHSGRIPISLETQAHIQECK--HPSVFOHGDNSFRLLFDV 303
Db 272 RHOELPDCYDFTLTITFDNKAHSGRIKISLDNDISIKECKDMHVSQIOKNTHYMMIFDA 331
QY 304 VVILTCSLFLLCARSLRGLQNEFVGMFWRQGRVLSLWERLEFVNGVILLVTSV 363
Db 332 FVILTCSLVILCARSVIRGLQIQEFVNFLLHYKKEVSQDMEFINGWYIWIISDI 391
QY 364 LTISGTIMKIGIEAKNLASYDVCSILLGTSTLLVWVGIRYLTFFHNYNLIATLRVALP 423
Db 392 LATVGSVLKWEIQAKSLTSYDVCSILLGTSTLWLVGIRYLGFFAKYNLLILTLQAALP 451
QY 424 SVMRFCCCVAVIYLVGFCGWTVLGPHYHVKFSLSMVSECLFSLINGDDMFVTFAMQAQ 483
Db 452 NVMRFCCCAAMIYLVGFCGWTVLGPHYHVKFSLSMVSECLFSLINGDDMFVTFAMQO- 510
QY 484 QGRSSVLWFLFSLYLSFISFIYVWLSFIALITGAYDTIKHPGGAGAESELOAYIAQ 543
Db 511 --KSLVWLFPSVYLYSFIYVWLSFIALITGAYDTIKHPGGAGAESELOAYIAQ 568
QY 544 QODSPTSGKFRGSGASLCCCGRDPSEHSLLVN 594

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QY 484 QGRSSLVWLFSSLYSLFSLFYMLSLFIALITGAYDTIKHPGGAGAESELOAYIAQ 543
Db 508 --KSYLVWLFSSLYSLFSLFYMLSLFIALITGAYDTIKHPGGAGAESELOAYIAQ 565
QY 544 QDSPTSGKFRGSGSACSLCC 567
Db 566 KDLFNSGKYLEDDPPGSLCC 589

RESULT 9
Q8CDB2 PRELIMINARY; PRT; 593 AA.
AC Q8CDB2;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE weakly similar to MUCOLIPIDIN (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK030819; BAC27146.1; -.
FT NON-TER
SQ SEQUENCE 593 AA; 68255 MW; F3708D6B5429E9BF CRC64;

Query Match 52.9%; Score 1623.5; DB 11; Length 593;
Best Local Similarity 55.4%; Pred. No. 3.9e-136;
Matches 312; Conservative 89; Mismatches 125; Indels 37; Gaps 5;

QY 7 PRGSETERLLTPNGYGTQAGSPAPPTPEEDLRRRLKYPFMSPCDKFRAGKPKL 66
Db 64 PSSSPSGLL-----EQMRRLKFFFMNPFCEKFWARGKPKWL 103

QY 67 MLQVVKLVTVQLIFGLSNQLAVTPRENTIAFRHLFLGYSOGADDTAAAYTREQLY 126
Db 104 AIQILKAMVTIQLVLEGLSNQWVAFKENTIAFKHLFKGMDMDTAYVTOSEY 163

QY 127 QAIHAVDQYALPDVSLGRIYVRGGDPWTNGSLGALCQRYHGHVDPANDTFDIDP 186
Db 164 DOIIFAVTQVQLQNIQSVGNHAYENKG---TKQSAMAIQHFYRGOTICPGNDTFDIDP 219

QY 187 MVTDCIQVDPPEPPPPDDLTLLSSSSYKNLTILKPKLVNVTIHPRLKTIINQSLI 246
Db 220 EVETECFLVPEDE-----DSHLGTFGENKUNLSLDPHLLTVLQFKLAINLQTVR 271

QY 247 NNEIPDCYTSVLTITFNKAHSGRIPISTQAHIOECK--HPSVFQHGDSNRLFLDVV 304
Db 272 HQELPCYDFLTITFNKAHSGRIKISLNDISIECKDWHVSGISQKNTHYMMIFDAF 331

QY 305 VILTCSLFLCARSLRGLLQNEFVGFWRGRVLSWERLBFNGWYLLVTSYDL 364
Db 332 VILTCLASLVLCARSLRGLLQNEFVGFWRGRVLSWERLBFNGWYLLVTSYDL 391

QY 365 TISGTINIKIGIEAKNLASVDVCSILLGTSTLLWVGVIYRLTFNHNINILATRLVALPS 424
Db 392 TIVCSVLKMELOAKSLTSDVCSILLGTSTLLWVGVIYRLGFPKYNLLILTLQALPN 451

QY 425 VMRFCCCVAVIYLCYFCGVIYKFRSLRSLVSWSECLFSLINGDDMFVTFPAAQAOQ 484
Db 452 VMRFCCCAAMVYLCYFCGVIYKFRSLRSLRNVSECLFSLINGDDMFSTFA---KKQ 508

QY 485 GRSSLVWLFSSLYSLFSLFYMLSLFIALITGAYDTIKHPGGAGAESELOAYIAQ 544

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Db 509 QKSYLVWLFSSLYSLFSLFYMLSLFIALITDTYETIKHYQODGFPTELKRFIARC 568
QY 545 QDSPTSGKFRGSGSACSLCC 567
Db 569 KDLFNSGKYLEDDPPGSLCC 591

RESULT 10
Q8TDDS PRELIMINARY; PRT; 553 AA.
AC Q8TDDS;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Mucolipin-3.
GN MCOLIN3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Falardeau J.L., Kennedy J.C., Acierno J.S., Slangenheut S.A.;
RT "Cloning of the MCOLIN3 gene.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF475085; AAL84622.1; -.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 553 AA; 64247 MW; 2E63DA196379F9E3 CRC64;

Query Match 52.9%; Score 1621; DB 4; Length 553;
Best Local Similarity 57.5%; Pred. No. 5.9e-136;
Matches 311; Conservative 87; Mismatches 121; Indels 22; Gaps 6;

QY 34 TPPEE-----DLRRRLKYPFMSPCDKFRAGKPKLQVVKLVTVQLIFGLSNQ 88
Db 26 TSPSEELLDDQWRKLLKFFMNPCEKFWARGKPKLAIQILKIMVTIQLVIFGLSNQ 85

QY 89 LAVTPRENTIAFRHLFLGYSOGADDTAAAYTREQLYQAIHAVDQYALPDVSLGRYA 148
Db 86 MVVAFKEENTIAFKHLFLKGYMDMDTAYVTSQSDVYDQILFAVQYQLYVNSVGNHA 145

QY 149 YVRGGDPWTNGSLGALCQRYHGHVDPANDTFDIDPVVTDICIQVDPPEPPPSDD 208
Db 146 YENKG---TKQSAMAIQHFYRGNIYPGNDTFDIDPEIETECFFVEPDE----PFHI 196

QY 209 LTLLESSSYKNLTILKPKLVNVTIHPRLKTIINQSLINNEIPDCYTSVLTITFNKAHS 268
Db 197 GTPAENK--LNLTLDFHLLTVLQFKLAINLQTVRHQELPCYDFTLTITFNKAHS 253

QY 269 GRIPISLETQAHIOECK--HPSVFQHGDSNRLFLDVVWILTCSLFLCARSLRGLL 326
Db 254 GRIPISLNDISIRECKDWHVSGISQKNTHYMMIFDAFVILTCLVSLILCIRSVIRGLQ 313

QY 327 QNEFVGFWRGRVLSWERLBFNGWYLLVTSQVLTISGTINIKIGIEAKNLASVDVC 386
Db 314 QOEFVNFLLHYKEVSDQMEFNGWYIMIIISLITIGSLKMEIOAKSLTSYDVC 373

QY 387 SILGTSTLLWVGVIYRLTFNHNINILATRLVALPSVMRFCCCVAVIYLCYFCGVI 446
Db 374 SILGTSTMLVGLVIRYLGFFAKYNLLILTLQALPNVIRFCCCAAMVYLCYFCGVI 433

QY 447 LGPHVFRSLVSWSECLFSLINGDDMFVTFPAAQAOQGRSSLVWLFSSLYSLFSLFI 506
Db 434 LGPHVDFRSLRNVSWSECLFSLINGDDMFATFAPKQQ---KSYLVWLFSSLYSLFI 490

QY 507 YMWLSLFIALTITGAYDTIKHPGGAGAESELOAYIAQODSPSTSGKFRGSGSACSLCC 566
Db 491 YMWLSLFIALTITYETIKHYQODGFPTELKRFIASECKDLPSGKYLEDDPPVSLFCC 550

QY 567 C 567

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Db      551 C 551
RESULT 11
Q9NV09 PRELIMINARY; PRT; 497 AA.
AC Q9NV09;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Hypothetical protein FLU11006.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Ariya M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagenari K., Masuno Y., Oshima A.;
RA "NEO human cDNA sequencing project.";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK001868; BAA91951.1; -.
DR EMBL; IPR002111; Cat channel TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
KW Hypothetical protein; ionic channel; Transmembrane..
SQ SEQUENCE 497 AA; 57739 MW; 3128395B50E5890D CRC64;

Query Match 45.5%; Score 1396; DB 4; Length 497;
Best Local Similarity 51.2%; Pred. No. 6.1e-116;
Matches 277; Conservative 78; Mismatches 108; Indels 78; Gaps 7;

QY 34 TPPEE-----DLRLKVFPMSPCKFRKGRKPKCKMLQVVKLVTVQLILFGLSNQ 88
Db      26 TSPSEALLEDDQRRKLFKFFNFNCPCKEFGWARKWKLAIQLIKTAMVTI----- 75

QY 89 LAVTREENTIAFRHLFLIGYSDGADDTFAAYTRQLYCAIFHAVDQVLAIPDVSLSGRYA 148
Db      76 -----QYLQYVNSVGNHA 89

QY 149 YVGGGDPWTNGSLALCQRYHGHVDPANDTFDIPMWVTDICQVDPPEPPPSDD 208
Db      90 YENKG---TKQSAVAICQHFYKRGNIYPCNDTFDIDPEIETECFVEPDE-----PPI 140

QY 209 LTLLESSSYKNTLTKFKHLVNVTHFRKLTINLQSLINNEIPDCYTSVLITFDNKAHS 268
Db      141 GTPAENK---LNLTDLFHLLTVELQKUKAINLQTVRHQELPDCYDFTLITFDNKAHS 197

QY 269 GRIPISLQAHIOECK--HPSVFQHGNSFLLFDVWVILFCSLFCARSILRGFL 326
Db      198 GRIKISLNDISIRBCKDWHVSSIQKNTYWMIFDAFVILTCLVSLILCIRSIVRIGLQ 257

QY 327 QNEFVGFMRQGRVLSLWERLEFVNGVILVTSVLTISCTIMKIGIEAKNLASYDVC 386
Db      258 QQEFVNFPLLHYKKEVSVDQEFVNGVIMTIISDILTIGSILKMEIQAKSLTSYDVC 317

QY 387 SILLGSTLLVWGVIRYITFEHNNILATLURVALPSVMRECCCVAVIYLGCFCGMIV 446
Db      318 SILLGSTLWLVGVIRYLCGFAKYNLLTILQALPNVIRCCCAANIYLGCFCGMIV 377

QY 447 LGPYHVKFRSLNVSCLFSLINGDDMFVTFPAAQOQGRSSLVWLFSQLYLSFISFI 506
Db      378 LGPYHDKFRSLNVSCLFSLINGDDMFATFAKMQO---KSLVWLFSGRIYLSFISFI 434

QY 507 YVLSLFIALTICAYDTIKHPGAGAESELOQYIAQCQDSPTSGKFRGSGSASLILCC 566
Db      435 YMLSLFIALTIDTYETIKQYQDQGFPELRTFISECKDLFNSGKYRLEDDPPVSLFCC 494

QY 567 C 567
Db      495 C 495

RESULT 12
Q81ZK6 PRELIMINARY; PRT; 538 AA.
ID Q81ZK6;
AC Q81ZK6;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Hypothetical protein FLU11006.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=22317414; PubMed=12403827;
RX Di Palma F., Belyantseva I.A., Kim H.J., Vogt T.F., Kachar B.,
RA Neben-Trauth K.;
RT "Mutations in Mcoln3 associated with deafness and pigmentation defects
RT in varitint-waddler (Va) mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14994-14999(2002).
DR EMBL; AY083533; AAM08926.1; -.
SQ SEQUENCE 538 AA; 62684 MW; 1BCCB92F8D6C83C4 CRC64;

Query Match 44.8%; Score 1374; DB 4; Length 538;
Best Local Similarity 48.9%; Pred. No. 6.2e-114;
Matches 268; Conservative 115; Mismatches 143; Indels 22; Gaps 8;

QY 37 EEDLRLRLKVFPMSPCKFRKGRKPKCKMLQVVKLVTVQLILFGLSNQIAVTFREE 96
Db      9 KEBCLEADLKVFPMSPCKFYKRRARQIPWKLGQILKIWMVTTQLVRFGLSNQLVAFKED 68

QY 97 NTIAPRHLFLIGYSDGADDTF--AAYTRQLYCAIFHAVDQVLAIPDVSLSGRYAVRG 154
Db      69 NTVAFKELFLKGYSGDEDDYSCSVYTQEDAYESIFFAINQYHQLKIDITLGLY---G 124

QY 155 DPTNGSGALCQRYHGHVDPANDTFDIPMWVTDICQVDPPEPPPSDDTLLES 214
Db      125 ENEDNRIQKLVKQHYKRGNTMFSNETLINDVDELDCVQLDLQLSKXPPD-----WKN 179

QY 215 SSSYKNTLTKFKHLVNVTHFRKLTINLQSLINNEIPDCYTSVLITFDNKAHSGRIPS 274
Db      180 SSFPR---LEFYRLQVLEISFHLKIGIDLQTIHSRELPCYVFQNTIIFDNKAHSGKIKY 236

QY 275 LETQAHIOECKHPSVF--QHGDNSFLLFDVWVILFCSLFCARSILRGFLQNEFVG 332
Db      237 FSDAKIECKDNLINFGSTQKQAQYVIVFDAFVIVCLASLILCTRSIVIALRLRRFLN 296

QY 333 FMRQGRVLSLWERLEFVNGVILVTSVLTISCTIMKIGIEAKNLASYDVCSTILGT 392
Db      297 FLEKYKRPVCDTQDQEFNGVIVLISDILMTIIGSILKMEIKAKNLNYDLCSIFLCT 356

QY 393 STLLVWGVIRYITFEHNNILATLURVALPSVMRECCCVAVIYLGCFCGMIVLGPYH 452
Db      357 STLLVWGVIRYILGYFQAYNVILTNQASLPKVLRFCAAGMIYLGTYTCGMIYLGPHYD 416

QY 453 KPSLSNVSCLFSLINGDDMFVTFPAAQOQGRSSLVWLFSQLYLSFISFIYVWLSL 512
Db      417 KFNELMTVAECLFSLVNGDDMFATFA--QIQQ--KSLVWLFSLRYLSFISFIYVWLSL 473

QY 513 FIALITGAYDTIKHPGAGAESELOQYIAQCQDSPTSGKFRGSGSASLILCCORDPS 572
Db      474 FIALITDSYDTIKKFFQNGFPETDLQEFLEKCS---SKEEYQKESAFSLICICRRRKES 530

QY 573 EHSLLVN 580
Db      531 DDHLIPIS 538

```

```

RESULT 13
QC03D3 PRELIMINARY; PRT; 538 AA.
ID QC03D3
AC QC03D3
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE 330002C04RIK protein (Mucolipin 2).
GN 330002C04RIK OR MCOLN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22317414; PubMed=12403827;
RA Di Palma F., Belyantseva I.A., Kim H.J., Vogt T.F., Kachar B.,
RA Noben-Trauth K.;
RT "Mutations in Mcoln3 associated with deafness and pigmentation defects
in varitint-waddler (Va) mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14994-14999(2002).
DR EMBL; AK019454; BAB31730.1; -
DR EMBL; AK014467; BAB29372.1; -
DR EMBL; AY083532; AAM08925.1; -
DR MGD; MGI:1915529; 330002C04RIK
DR InterPro; IPR002111; Cat_channel_TpPL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 538 AA; 62269 MW; 9C35081FE96A628B CRC64;

Query Match 43.5%; Score 1335; DB 11; Length 538;
Best Local Similarity 49.3%; Pred. No. 1.9e-110;
Matches 271; Conservative 101; Mismatches 150; Indels 28; Gaps 9;

Qy 38 EEDLRRLKVFMSPCDKFRAGKRPCKLMQVVKLVVTVQILVGLSNQLAVTFREEN 97
Db 10 EECRLDLKVFMSPEKRYARRQIPWKLGLQILKLVMTTQIVFGLSNQLVAFKEDN 69
Qy 98 TIAFRHLFLIGYSDGADDTFAA--YTRQLYQAIHAVDQYALPDVSLGRVAYVRGGD 155
Db 70 TVAFKHLFLKFGSGVDEDDYSCSIYQNTYIESIFFAIKQYRHLKNISLATGY----GE 125
Qy 156 PWTNGSGLALCQRYHGRVDPANDTFDIDPMVVTDCIQVDPPPPPPPSDDTLLESS 215
Db 126 SEDNRTGLKVKCKOYKTYTGAMFSSNETLNDSDIETDCIHLDLQVLTTEP-----BDW 177

RESULT 14
Q8K595 PRELIMINARY; PRT; 566 AA.
ID Q8K595
AC Q8K595;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Mucolipin-2.
GN 330002C04RIK OR MCOLN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Kennedy J.C., Falardeau J.L., Acierno J.S. Jr., Slaugenhaupt S.A.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF503575; AAM28596.1; -
DR MGD; MGI:1915529; 330002C04RIK.
DR InterPro; IPR002111; Cat_channel_TpPL.
DR SEQUENCE 566 AA; 65445 MW; 314CEC662B3BDC07 CRC64;

Query Match 43.5%; Score 1335; DB 11; Length 566;
Best Local Similarity 49.3%; Pred. No. 2e-110;
Matches 271; Conservative 101; Mismatches 150; Indels 28; Gaps 9;

Qy 38 EEDLRRLKVFMSPCDKFRAGKRPCKLMQVVKLVVTVQILVGLSNQLAVTFREEN 97
Db 38 EECRLDLKVFMSPEKRYARRQIPWKLGLQILKLVMTTQIVFGLSNQLVAFKEDN 97
Qy 98 TIAFRHLFLIGYSDGADDTFAA--YTRQLYQAIHAVDQYALPDVSLGRVAYVRGGD 155
Db 98 TVAFKHLFLKFGSGVDEDDYSCSIYQNTYIESIFFAIKQYRHLKNISLATGY----GE 153
Qy 156 PWTNGSGLALCQRYHGRVDPANDTFDIDPMVVTDCIQVDPPPPPPPSDDTLLESS 215
Db 154 SEDNRTGLKVKCKOYKTYTGAMFSSNETLNDSDIETDCIHLDLQVLTTEP-----EDW 205
Qy 216 SSYKNLTILKFKLVNVTIHFRLKTNLQSLINNEIPDCYTFSVLITFDNKAHSGRIPISL 275
Db 206 AQTSFFELDFYRLVQVDISFALKGIDLQAVHSREIPDCYLFQNTITFDNKAHSGRIPISL 265
Qy 276 ETQAHIQECKHPSVFQHGDS--FRLLFDVVVILTCSLFLLCARSLRGLLQNEFVG 333

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 27, 2003, 12:34:37 ; Search time 75 Seconds
(without alignments)
1227.485 Million cell updates/sec

Title: US-09-851-494B-3

Perfect score: 3067

Sequence: 1 WTAPAGRSGSERLITPNPCSLLCCGRDPSEHSLIVN 580

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length DB	ID	Description
1	3067	100.0	580	22	Human membrane ass
2	3067	100.0	580	23	Human TLCC-2 prote
3	3067	100.0	580	23	Human TRP-like cal
4	2685	87.5	511	23	Human polypeptide
5	2661	86.8	511	21	Human secreted pro
6	1396	45.5	497	22	Human protein sequ
7	1376	44.9	538	24	Human NOV9c CG9070
8	1368	44.6	566	24	Human NOV9d CG9070
9	1367	44.6	544	24	Human NOV9b CG9070

10	1311	42.7	540	24	ABU12051	Human NOV9a CG9070
11	1236	40.0	255	23	ABW2389	Murine protein iso
12	1025.5	33.4	652	22	ABW1675	Drosophila melanog
13	979	31.9	191	22	ABG01744	Novel human diagn
14	689	22.5	193	22	AAU00503	Human TANGO 480 pr
15	627	20.4	154	23	ABW89290	Human polypeptide
16	599.5	19.5	164	22	ABW11279	Human secreted pro
17	551	18.0	600	22	ABG01746	Novel human diagn
18	507.5	16.5	106	22	ABG25123	Novel human diagn
19	308	10.0	1120	22	ABG25135	Novel human diagn
20	293	9.6	603	22	ABG27454	Novel human diagn
21	281.5	9.2	69	22	ABG57092	Human liver peptid
22	281.5	9.2	69	22	AAW63524	Human brain expres
23	281.5	9.2	69	22	AAW35448	Peptide #9485 enco
24	259.5	8.5	120	22	AAW89441	Human immune/haema
25	207.5	6.8	642	22	ABG08087	Novel human diagn
26	161.5	5.3	897	22	ABW62418	Drosophila melanog
27	152.5	5.0	621	23	AAU98515	Mouse Polycystatin-2
28	152.5	5.0	966	23	ABW07819	Mouse polycystatic k
29	152.5	5.0	966	23	AAW51861	Murine polycystic
30	150.5	4.9	76	22	ABG58066	Human liver peptid
31	150.5	4.9	76	22	ABW42654	Peptide #10160 enc
32	150.5	4.9	76	22	ABW25997	Protein #7996 enco
33	150.5	4.9	76	22	AAW63544	Human brain expres
34	150.5	4.9	76	22	AAW76359	Human bone marrow
35	150.5	4.9	76	22	AAW36467	Human peptide enco
36	150.5	4.9	76	23	ABG45651	Human acrosome rea
37	147.5	4.8	2253	21	AAV44301	Human polypeptide
38	146	4.8	469	22	AAW41866	Peptide #5191 enco
39	141.5	4.6	224	22	AAW31154	Human polycystatic k
40	140.5	4.6	805	23	AAE25587	Mouse acrosome rea
41	140	4.6	2126	21	AAV44302	Amino acid sequenc
42	138	4.5	866	22	AAW68448	Human Polycystatin-L
43	136.5	4.5	805	21	AAV70245	Human liver peptid
44	127	4.1	53	22	ABG56554	Peptide #8717 enco
45	127	4.1	53	22	ABW41211	

ALIGNMENTS

RESULT 1
AAB74707
ID AAB74707 standard; Protein; 580 AA.

XX AAB74707;
AC AAB74707;
XX
DT 12-JUN-2001 (first entry)

DE Human membrane associated protein MEMAP-13.

XX Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.

XX Homo sapiens.

XX WO200112662-A2.

XX 22-FEB-2001.

XX 14-AUG-2000; 2000WO-US22315.

XX 17-AUG-1999; 99US-0149641.

XX 09-NOV-1999; 99US-0164203.

XX (INCY-) INCYTE GENOMICS INC.

XX Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;

PI Baughn MR, Lu DAM, Patterson C;

```
XX WPI; 2001-169860/17.
DR N-PSDB; AAF81753.
XX
XX Isolated polypeptide with a human membrane associated protein sequence
PT is useful for the diagnosis, prevention and treatment of cell
PT proliferative, autoimmune/inflammatory, neurological and
PT gastrointestinal disorders -
XX
XX Claim 1; Page 125-126; 173pp; English.
XX
XX AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAF81749S to AAF81747S. MEMAPs have cytosolic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrhetic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders
CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated
CC with MEMAP.
XX
XX Sequence 580 AA;
XX
XX Query Match 100.0%; Score 3067; DB 22; Length 580;
XX Best Local Similarity 100.0%; Pred. NO. 0;
XX Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRLKYFFMSPCDKFRAGK 60
DB 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRLKYFFMSPCDKFRAGK 60
QY 61 RKCEKLMQVVKILVTVQILFGLSNQLAVTPRENTIAFRHLFLGLYSDGADDTFAAY 120
DB 61 RKCEKLMQVVKILVTVQILFGLSNQLAVTPRENTIAFRHLFLGLYSDGADDTFAAY 120
QY 121 TRQLYQAI FHAVDQYALPDVSLGRVAYVRGGDPWTNGSLALCORYYHRGHVDPAND 180
DB 121 TRQLYQAI FHAVDQYALPDVSLGRVAYVRGGDPWTNGSLALCORYYHRGHVDPAND 180
QY 181 TFDIDPMVVTDCIQVDPPEPPPPSDLLLESSSYKNLTKFKHLVNVTHFRKTI 240
DB 181 TFDIDPMVVTDCIQVDPPEPPPPSDLLLESSSYKNLTKFKHLVNVTHFRKTI 240
QY 241 NLOSLINNETPCYTFVSLTFDNKAHSGRIPISLETOAHIOCKHPSPVFQHGDNFRL 300
DB 241 NLOSLINNETPCYTFVSLTFDNKAHSGRIPISLETOAHIOCKHPSPVFQHGDNFRL 300
QY 301 FDVVILTCSLFLLCARSLLRGFLLONEFVGFMRQGRVLSLWELFVNGWYILLVT 360
DB 301 FDVVILTCSLFLLCARSLLRGFLLONEFVGFMRQGRVLSLWELFVNGWYILLVT 360
QY 361 SDVLTISGTTMKIGIEAKNLASDVCSILLGTSLLVWVGVIYRLTFPHNVIILATLRV 420
DB 361 SDVLTISGTTMKIGIEAKNLASDVCSILLGTSLLVWVGVIYRLTFPHNVIILATLRV 420
QY 421 ALPSVMRFCCCAVYILGYFCGQWILGPYHVRFSLSMVSECLFSLINGDDMFVTFAM 480
DB 421 ALPSVMRFCCCAVYILGYFCGQWILGPYHVRFSLSMVSECLFSLINGDDMFVTFAM 480
QY 481 QAQGRSSLVWLFSQLYXSFISLFIYMWLSFIALTITGAYDTIKHPGGAGABESELQAY 540
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DB 481 QAQGRSSLVWLFSQLYXSFISLFIYMWLSFIALTITGAYDTIKHPGGAGABESELQAY 540
QY 541 IAQCQSPSTSGKFRGSGSACSLCCCGRDPSPSEHSLVNV 580
DB 541 IAQCQSPSTSGKFRGSGSACSLCCCGRDPSPSEHSLVNV 580
RESULT 2
ABB07816
ID: ABB07816 standard; Protein; 580 AA.
XX
XX ABB07816;
XX
DT 03-JUL-2002 (first entry)
XX
DE Human TLCC-2 protein.
XX
XX Transient receptor potential like calcium channel; TRP; TLCC-2; human;
XX neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;
XX KW cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy;
XX calcium signaling.
XX
XX Homo sapiens.
XX
XX US2002035056-A1.
XX
XX 21-MAR-2002.
XX
XX 06-APR-2001; 2001US-0828466.
XX
XX 07-APR-2000; 2000US-0544797.
XX
XX (CURTIS R A J.
XX (SILO/) SILOS-SANTIAGO I.
XX
XX Curtis RAJ, Silos-Santiago I;
XX
XX WPI; 2002-338931/37.
XX
XX N-PSDB; ABL40754, ABL40755.
XX
XX New nucleic acid designated TLCC-2 encodes a transient receptor
XX potential-like calcium channel and is useful to diagnose and treat pain
XX disorders and central nervous system neurodegenerative and neurological
XX disorders -
XX
XX Claim 7; Fig 1A-B; 70pp; English.
XX
XX The invention relates to a novel transient receptor potential (TRP)-like
XX calcium channel, designated TLCC-2 and polynucleotides encoding the
XX TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The
XX TLCC-2 polypeptide, polynucleotides and modulators are useful for
XX treating central nervous system disorders such as neurodegenerative
XX disorders for example Alzheimer's disease, Parkinson's disease, multiple
XX sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy,
XX epilepsy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial
XX infantile convulsions, paroxysmal choreoathetosis, psychiatric disorders
XX such as depression, anxiety, schizophrenia, psychoses, mania or phobic
XX disorders, learning or memory disorders such as amnesia, age-related
XX memory loss, or a neurological disorder such as migraine. The molecules
XX are also useful to treat a pain disorder. The present sequence represents
XX the human TLCC-2 polypeptide.
XX
XX Sequence 580 AA;
XX
XX Query Match 100.0%; Score 3067; DB 23; Length 580;
XX Best Local Similarity 100.0%; Pred. NO. 0;
XX Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRLKYFFMSPCDKFRAGK 60
DB 1 MTAPAGPRGSETERLLTPNPGYGTQAGSPAPPTPEEDLRRLKYFFMSPCDKFRAGK 60
```

Qy	61	RKPC	KMLQ	VVKIL	VVTQ	LIFGL	SNQ	LAVT	FR	EBNT	IA	FRH	LFG	YSG	DADT	FAAY	120	
Db	61	RKPC	KMLQ	VVKIL	VVTQ	LIFGL	SNQ	LAVT	FR	EBNT	IA	FRH	LFG	YSG	DADT	FAAY	120	
Qy	121	TREQ	LYQA	IF	HA	VOYL	AL	PD	VS	LGR	YAV	RG	GD	PW	TS	GS	LAL	180
Db	121	TREQ	LYQA	IF	HA	VOYL	AL	PD	VS	LGR	YAV	RG	GD	PW	TS	GS	LAL	180
Qy	181	TFD	ID	PW	VT	DCI	Q	VD	PER	PP	PP	SD	DL	T	LE	SS	SY	240
Db	181	TFD	ID	PW	VT	DCI	Q	VD	PER	PP	PP	SD	DL	T	LE	SS	SY	240
Qy	241	NQ	SL	IN	NEI	P	DC	Y	T	F	S	V	L	I	T	F	D	300
Db	241	NQ	SL	IN	NEI	P	DC	Y	T	F	S	V	L	I	T	F	D	300
Qy	301	PD	V	V	I	L	T	C	S	L	F	L	C	A	R	S	L	360
Db	301	PD	V	V	I	L	T	C	S	L	F	L	C	A	R	S	L	360
Qy	361	S	D	V	L	T	I	S	G	T	I	K	I	G	I	E	A	420
Db	361	S	D	V	L	T	I	S	G	T	I	K	I	G	I	E	A	420
Qy	421	A	P	S	W	M	F	C	C	C	V	A	V	I	Y	G	C	480
Db	421	A	P	S	W	M	F	C	C	C	V	A	V	I	Y	G	C	480
Qy	481	Q	A	O	G	R	S	S	L	V	M	F	S	O	L	Y	P	540
Db	481	Q	A	O	G	R	S	S	L	V	M	F	S	O	L	Y	P	540
Qy	541	I	A	O	C	D	S	P	T	G	K	F	R	G	S	A	C	580
Db	541	I	A	O	C	D	S	P	T	G	K	F	R	G	S	A	C	580

RESULT 3	
AAM51858	
ID	AAM51858 standard; Protein; 580 AA.
XX	
AC	AAM51858;
XX	
DT	29-JAN-2002 (first entry)
XX	
DE	Human TRP-like calcium channel TLCC-2.
XX	
KW	Human; TLCC-2; TRP-like calcium channel; membrane excitability;
KW	nociception; nootropic; neuroprotective; antiparkinsonian; cytostatic;
KW	hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;
KW	Parkinson's disease; Huntington's disease; multiple sclerosis;
KW	Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
KW	neuroleptic; gene therapy; Alzheimer's disease; CNS disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200177331-A1.
XX	
XX	18-OCT-2001.
FD	
XX	
PF	06-APR-2001; 2001WO-US11442.
XX	
PF	07-APR-2000; 2000US-0544797.
XX	
PR	(MILL-) MILLENIUM PHARM INC.
XX	
PI	Curtis RAJ, Silos-Santiago I;
XX	
XX	WPI; 2002-010913/01.
DR	N-PSDB; AAI17699, AAI17700.
XX	
PT	Novel isolated human transient receptor potential-like calcium channel
PT	protein-2 useful for treating Alzheimer's disease, depression, amnesia

PT pain disorder, and cancer -
 xx Claim 7; Fig 1; 148pp; English.
 xx
 xx
 CC The present invention relates to the protein and coding sequences of
 CC human transient receptor potential (TRP)-like calcium channel protein-2
 CC (TLCC-2). The sequences can be used in the treatment of TLCC-2 related
 CC disorders, including central nervous system disorders such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis,
 CC Gilles de la Tourette's syndrome, autonomic function disorders, learning
 CC or memory disorders, pain disorders and disorders of cellular
 CC proliferation, including cancer. The present sequence is the TLCC-2
 CC protein.
 xx
 xx
 SQ Sequence 580 AA;

 Query Match 100.0%; Score 3067; DB 23; Length 580;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0

 Qy 1 MTPAGPRGSEIRLLTPNGYGTQAGSPAPPTPEEDLRRLKLYFFMSPCDKPKAG 60
 Db 1 MTPAGPRGSEIRLLTPNGYGTQAGSPAPPTPEEDLRRLKLYFFMSPCDKPKAG 60

 Qy 61 RPKCLMLQWKILVTVQLILFGLSNQLAVTFRENTIAFRHLFLGYSDGADDTFAAY 120
 Db 61 RPKCLMLQWKILVTVQLILFGLSNQLAVTFRENTIAFRHLFLGYSDGADDTFAAY 120

 Qy 121 TREOLYQALFHAVDOYLALPDVSLGRVAYVRGGDPWTNGSLGALCQRYVHRGHVDPAND 180
 Db 121 TREOLYQALFHAVDOYLALPDVSLGRVAYVRGGDPWTNGSLGALCQRYVHRGHVDPAND 180

 Qy 181 TFDIDPMVVTDCIQVDPPERPPPSDDLTLESSSVKNLTLPKHLVNVTHFRKLT 240
 Db 181 TFDIDPMVVTDCIQVDPPERPPPSDDLTLESSSVKNLTLPKHLVNVTHFRKLT 240

 Qy 241 NLQSLINNEIPDCTYFSVLITFDNKAHSGRIPI SLETOAHIQECKHPSVFHGDNQFRLL 300
 Db 241 NLQSLINNEIPDCTYFSVLITFDNKAHSGRIPI SLETOAHIQECKHPSVFHGDNQFRLL 300

 Qy 301 FDVWVILTCSLSFLLCARSLRGLFLQNEFVGFMWRQGRVVISLWERLEFVNGWYILLVT 360
 Db 301 FDVWVILTCSLSFLLCARSLRGLFLQNEFVGFMWRQGRVVISLWERLEFVNGWYILLVT 360

 Qy 361 SDVLITSGTIMKIGIEAKNLASYDVCSILGTSTLLVWGVIRYLTPFHNYNILIALRV 420
 Db 361 SDVLITSGTIMKIGIEAKNLASYDVCSILGTSTLLVWGVIRYLTPFHNYNILIALRV 420

 Qy 421 ALPSVMRFCCCVAVILGYCFCGWILGPHVHFRSLSNVSECLFSLINGDDMFVTPAAM 480
 Db 421 ALPSVMRFCCCVAVILGYCFCGWILGPHVHFRSLSNVSECLFSLINGDDMFVTPAAM 480

 Qy 481 QAOQGRSLVWLFSQLYLYGFISLFIYVNLISLFIALTITGAYDTIKHPGAGAESESLQAY 540
 Db 481 QAOQGRSLVWLFSQLYLYGFISLFIYVNLISLFIALTITGAYDTIKHPGAGAESESLQAY 540

 Qy 541 TAOQODSPSTGKFRGSGSACSLCCCGRDPSEHSLLVN 580
 Db 541 TAOQODSPSTGKFRGSGSACSLCCCGRDPSEHSLLVN 580

RESULT 4	
ABB89949	
ID ABB89949 standard; Protein; 511 AA.	
XX	
XX	
AC ABB89949;	
XX	
XX	
DT 24-MAY-2002 (first entry)	
XX	
XX	
DE Human polypeptide SEQ ID NO 2325.	
DE	
XX	
XX	
KW Cytostatic; immunosuppressive; nontropic; neuroprotective; antiviral;	
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;	

PT Novel isolated human transient receptor potential-like calcium channel protein-2 useful for treating Alzheimer's disease, depression, amnesia,

KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW ciliant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX Homo sapiens.
 OS WO200190304-A2.
 XX PD 29-NOV-2001.
 XX XX 18-MAY-2001; 2001WO-US16450.
 XX PF 19-MAY-2000; 2000US-205515P.
 XX PR (HUMA-) HUMAN GENOME SCI INC.
 XX PA Birse CE, Rosen CA;
 XX PI WPI: 2002-122018/16.
 XX DR N-PSDB; ABL90358.
 XX DR Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders -
 XX PS Claim 11; SEQ ID NO 2325; 2081pp + Sequence Listing; English.
 XX CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABL89040-ABL90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX XX Sequence 511 AA;
 Query Match 87.5%; Score 2685; DB 23; Length 511;
 Best Local Similarity 99.8%; Pred. No. 3.2e-281;
 Matches 510; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 70 VVKILVTVQLILFGLSNQLAVTFRENTIAFRHLFLGYSYGADTTFAAYTREQLYQAI 129
 Db 1 MVKILVTVQLILFGLSNQLAVTFRENTIAFRHLFLGYSYGADTTFAAYTREQLYQAI 60
 QY 130 FRAVDQYALPDVSLGRYAYVRGGDPWTNGSLALCQRYRGRHVDPAFTDIDPMV 189
 Db 61 FRAVDQYALPDVSLGRYAYVRGGDPWTNGSLALCQRYRGRHVDPAFTDIDPMV 120
 QY 190 TDCIQVDPPERPPPPDDTLLESSSSYKNTLTKFKHLVNTTIFRLKTNLQSLINNE 249
 Db 121 TDCIQVDPPERPPPPDDTLLESSSSYKNTLTKFKHLVNTTIFRLKTNLQSLINNE 180
 QY 250 IPDCYTFSVLITFDNKAHSGRIPISLETQAHQIECKHPSVFQHGNSFLLFDVVILTC 309
 Db 181 IPDCYTFSVLITFDNKAHSGRIPISLETQAHQIECKHPSVFQHGNSFLLFDVVILTC 240
 QY 310 SLSEFLCARSLRGLFLQNEFVCFMWRQRGRVLSLWERLEFVNGWILLVTSVLTISGT 369
 Db 241 SLSEFLCARSLRGLFLQNEFVCFMWRQRGRVLSLWERLEFVNGWILLVTSVLTISGT 300

QY 370 IMKIGIEAKNLASVDVCSILLGTSTLLVWVGIRYLTFPHNYNILLIATRLVALPSVMFRC 429
 Db 301 IMKIGIEAKNLASVDVCSILLGTSTLLVWVGIRYLTFPHNYNILLIATRLVALPSVMFRC 360
 QY 430 CCVAVIYLGYPGCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFANMAOQGRSSL 489
 Db 361 CCVAVIYLGYPGCGWIVLGPYHVKFRSLSMVSECLFSLINGDDMFVTFANMAOQGRSSL 420
 QY 490 VMLFSQLYLSFISLFIYMWLSLFIATITGAYDTIKHPGAGAESELSQAYIAQCDSPT 549
 Db 421 VMLFSQLYLSFISLFIYMWLSLFIATITGAYDTIKHPGAGAESELSQAYIAQCDSPT 480
 QY 550 SGKFRGSGSACSLCCCGRDPSEHSLLVN 580
 Db 481 SGKFRGSGSACSLCCCGRDPSEHSLLVN 511
 RESULT 5
 AAB08906
 ID AAB08906 standard; Protein; 511 AA.
 XX
 AC AAB08906;
 XX
 DT 30-AUG-2000 (first entry)
 DE
 DE Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.
 XX
 XX Human; secreted protein; cytostatic; anti-proliferative; vulnery;
 KW immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis;
 KW hyperproliferative disorder; infectious disease; tissue regeneration;
 KW screening; food additive; preservative; wound healing;
 KW hyper-vascular disease.
 OS Homo sapiens.
 XX WO200017222-A1.
 XX 30-MAR-2000.
 XX 22-SEP-1999; 99WO-US22012.
 XX 23-SEP-1998; 98US-0101546.
 PR 02-OCT-1998; 98US-0102895.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Rosen CA, Duan RD, Shi Y, Lafleur DW, Young PE, Ni J;
 PI Komatsoulis G, Endress GA, Soppet DR;
 XX WPI: 2000-283538/24.
 DR N-PSDB; AAA39067.
 XX Human secreted proteins and coding sequences useful in diagnostic and
 PT therapeutic methods for disorders such as immune system or
 PT proliferative disorders, related to the proteins -
 XX Claim 11; Page 362-363; 416pp; English.
 XX The polynucleotide sequences given in AAA39052 to AAA39088 encode the
 CC human secreted proteins given in AAB08891 to AAB08984. The human secreted
 CC proteins can have activities based on the tissues and cells they are
 CC expressed in. Examples of the activities are: cytostatic;
 CC anti-proliferative; immunosuppressive; antibacterial; and vulnery. The
 CC secreted proteins and their related polynucleotide sequences are useful
 CC for diagnostic and therapeutic methods useful for diagnosing and treating
 CC disorders related to the secreted proteins. The proteins, and
 CC polynucleotide sequences may be useful for treating disorders of the
 CC immune system, hyperproliferative disorders, infectious disease,
 CC regeneration of tissues, for chemotaxis and for screening molecules that
 CC bind to the proteins. The proteins or polynucleotide sequences may be
 CC used as food additives or preservatives, to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, co-factors or other nutritional components. Agonists or

CC antagonists of the proteins may be used to prevent scar tissue growth
CC during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051
CC and ABA08990 are sequences used in the exemplification of the present
CC invention.

Sequence 511 AA;

Query Match 86.8%; Score 2661; DB 21; Length 511;
Best Local Similarity 99.0%;
Pred. No. 1.3e-278;
Matches 506; Conservative 1; Mismatches 4; Indels 0

QY		70	VVKILVTVQIILFGLSNOLAVTFREENTIAFRHLFLLLGYSGDADTFAAYTREQLYOAI	129
Db	:	1	MVKILVTVQIILFGLSNOLAVTFREENTIAFRHLFLLLGYSGDADTFAAYTREQLYOAI	60
QY		130	FHAVDQYLALPDVSLGRVAYVRGGDPWTNGSGLALCORYHRGHVDPAANDTFDIDPMVV	189
Db		61	FHAVDQYLALPDVSLGRVAYVRGGDPWTNGSGLALCORYHRGHVDPAANDTFDIDPMVV	120
QY		190	TDCIQVDPPERP PPPPDDLTILESSSYKXNLTLPFKHKLNVNTIHFRUKTNLQSLINNE	249
Db		121	TDCIQVDPPERPPXPSPDDLTILESSSYKYULTPFKHKLNVNTIHFRUKTNLQSLINNE	180
QY		250	IPDCYTSSLITFDNKHAHSRIPISLETOAHIOECKHPVSFOHGNSPRLFFDVVVILTCT	309
Db		181	IPDCYTSSLITFDNKHAHSRIPISLETOAHIOECKHPVSFOHGNSPRLFFDVVVILTCT	240
QY		310	SLSFLLCARSLLRGFLLONEVFVGPMWRQGRGVISLWERLEFVNGWYILLVTSDVLITSGT	369
Db		241	SLSFLLCARSLLRGFLLQNEFVGPMWRQGRGVISLWERLEFVNGWYILLVTSDVLITSGT	300
QY		370	IMKIGIEAKNLASVDVCILLGTSLLLVMVGVIYLTTFHNVNILIALTRVALPSWMRFC	429
Db		301	IMKIGIEAKNLASVDVCILLGTSLLLVMVGVIYLTTFHNVNILIALTRVALPSWMRFC	360
QY		430	CCVAIVLYGCFCGWIVLGPVHVAFRSLSMWSECLFSLINGDDMFVTTAAQAOQGRSSL	489
Db		361	CCAIVLYGCFCGWIVLGPVHVAFRSLSMWSECLFSLINGDDMFVTTAAQAOQGRSSL	420
QY		490	VWLPSQYLYSFISLFYVWLVSFLIALITGAYDIKHFGAGABESELQVIAQCQDSPT	549
Db		421	VWLPSQYLYSFISLFYVWLVSFLIALITGAYDIKHFGAGABESELQVIAQCQDSPT	480
QY		550	SGFRRSGGSACSLLCGCCRDPPSEHSLLVN	580
Db		481	SGFRRGSARACSLLCGCCRDPPSEHSLLVN	511

RESULT 6

AAB93412
ID AAB93412 standard; protein; 497 AA.

AC AAB93412;

26-JUN-2001 (first entry)

XX
DE Human protein sequence SEQ ID NO:12616.

Human; primer; detection; diagnosis; antisense therapy; gene therapy.

OS Homo sapiens.

XX
PN
EP1074617-A2

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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09270TTO-350000Z , 0000Z EOC

PR	29-JUL-1999;	99JP-0248036.
PR	27-AUG-1999:	99JP-0300253

11-JAN-2000; 2000JP-0118776.

PR 09-JUN-2000; 2000JP-0241899.

(HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

Claim 8; SEQ ID 12616; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to a complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence	497 AA
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99	99
100	100

Query Match	45.5%	Score 1396;	DB 22;	Length 497;
Best Local Similarity	51.2%;	Pred. No. 1.2e-141;		
Matches 277;	Conservative 78;	Mismatches 108;	Indels 78;	Gaps 7
QY	34	TPPEBE-----DLRRRLKYPFMSPCDPRAKGRKPKMLQVVKILVVTVOLILFGLSNQ	148	
Db	26	TPSEELLEQMERKULKPFPMNCEKFWAGRKPKMLAIQILKIAMVTI-----	75	
QY	89	LAVTPRENTIAPRHLFLGLGSDGADDTFAAYTREQLYQAI PHAVQYALPDPVSLGRYA	148	
Db	76	-----CYLQLYNVSVGNHA	89	
QY	149	YVRGGDPWTNGSLALCORYHRGHVDPANDTFDIDPVVVTDCIOVDPPERPPPSDD	208	
Db	90	YENKG---TKQSAMAICQHFYKGNIIYPCGNDIFDIDPEIETECFFVEPDE-----PPHI	140	
QY	209	LTLESSSYXALTLEKHLVWVTHIHLRTKINLOSLINNEIDCVTFSVLTFDNKAHS	268	
Db	141	GTPAENK---LNLTLDFHRLTLTVELOFKLAINLQTVRHOELPDCYDFTLTITFDNKAHS	197	
QY	269	GRIPISLETQAHOECK--HPSVFQHCDSFRLFDVWVILICSLFCLCARSLRGFL	326	
Db	198	GRKISLNDISIRCKDMHVSQSIQKNTHYMMIDFAVILITCLVSLIICIRSVIRGLQ	257	
QY	327	QNEFVGFWMRQGRVLSLWERLEFVNGWYILLVTSDVLTISGTFIMKIGTEAKNLASYDC	386	
Db	258	QOEFWNFLLHYKKEVSDQMEFVNGWYIMIIISDILIIISILKWEIQAKLSISYDC	317	
QY	387	SILIGTSTLLVWGVIRYILTPFFHNYNIIATLRVALPSVRFCCCVAVIYLGVCFCGMV	446	
Db	318	SILIGTSTMLVGLVIRYLGFPAKYNLLIITLQALPNVIRFCCCAAMIYLGVCFCGMV	377	
QY	447	LGPHVHVFRSLSMVSECLFSLNGDDMFVTFPAAQOQGRSSLWLWFSOLHYFSISLFI	506	


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Db          531 DDHLIPIS 538
          :::::
RESULT 8
ABU12054
ID   ABU12054 standard; Protein; 566 AA.
AC   ABU12054;
XX
DT   19-FEB-2003 (first entry)
XX
DE   Human NOV9d CG90709-04 protein SEQ ID 28.
XX
KW   NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW   metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiac;
KW   antilipemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW   cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW   anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
KW   Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW   metabolic syndrome X; wasting disease.
XX
OS   Homo sapiens.
XX
PN   WO200281625-A2.
XX
PD   17-OCT-2002.
XX
PF   03-APR-2002; 2002WO-US10366.
XX
PR   03-APR-2001; 2001US-281086P.
PR   05-APR-2001; 2001US-281906P.
PR   06-APR-2001; 2001US-282020P.
PR   10-APR-2001; 2001US-282930P.
PR   12-APR-2001; 2001US-283444P.
PR   12-APR-2001; 2001US-283512P.
PR   13-APR-2001; 2001US-283657P.
PR   13-APR-2001; 2001US-283678P.
PR   13-APR-2001; 2001US-283710P.
PR   17-APR-2001; 2001US-284234P.
PR   19-APR-2001; 2001US-285325P.
PR   20-APR-2001; 2001US-285381P.
PR   24-APR-2001; 2001US-286068P.
PR   25-APR-2001; 2001US-286292P.
PR   07-JUN-2001; 2001US-286692P.
PR   26-JUN-2001; 2001US-300883P.
PR   08-AUG-2001; 2001US-311003P.
PR   13-AUG-2001; 2001US-311973P.
PR   16-AUG-2001; 2001US-312901P.
PR   14-SEP-2001; 2001US-322283P.
PR   05-OCT-2001; 2001US-327448P.
PR   31-DEC-2001; 2001US-345734P.
PR   03-JAN-2002; 2002US-345755P.
PR   04-FEB-2002; 2002US-354391P.
PR   02-APR-2002; 2002US-0114153.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson G;
PI   Guo X, Gerlach V, Casman SU, Boldog FL, Li L, Zerkhusen BD;
PI   Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM;
PI   Patturajan M, Miller CE, Taupier RJ, Hayes MP, Ju J, Peyman JA;
PI   Catterton E, MacDougall JR, Edinger SR, Stone DJ, Mazur A;
XX
WPI; 2003-046862/04.
DR   N-PSDB; ABX56274.
XX
PT   New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT   atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT   disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT   cancer.
XX
PS   Claim 1; Page 113; 425pp; English.

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```

XX This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipemic, cytostatic, nootropic,
CC cardiac and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC and portions of the polynucleotides encoding the NOVX polypeptide. Fragments
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, hematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306.
XX
SQ Sequence 566 AA;

```

```

Query Match          44.8%; Score 1368; DB 24; Length 566;
Best Local Similarity 48.7%; Pred. No. 1.6e-138;
Matches 267; Conservative 115; Mismatches 144; Indels 22; Gaps 8;

```

```

QY 37 EEDLRRLKFFMSPCDKFRAGKRPCKMLQVKKLVVTVQLILFGLNQLAVTFREE 96
DB 37 KECLREDLKFYCMSPCEKYARRQIPWKLGLQILKIVMWVTVQLVFRGLNQLVAFKED 96
QY 97 NTIAFRHLFLGLGYSGDADTF--AAYTREQLYQAIHFAVDQYLALPDVSLGRYAYVGGG 154
DB 97 NTVAFKHLFLKGYSGDDEDDYSCSVTQEDAYESIFAINQYHQLDITIGTGLY----G 152
QY 155 DPWTNGSLALCORYYRHGHVDPANDTFDIDPMVVTDCIQVDPPEPPPPDDLTLES 214
DB 153 ENEDNRIGLKVKQHYKGTMPFSNETLNDVDLDCVQLDQLDLSKKFPD-----WKN 207
QY 215 SSSYKNLTAKFKLVNVTIHFRLKTNLOSILNNEIPDCVTFSLVITFDNKAHSGRIPIS 274
DB 208 SSFPR---LEFYRLQLVEISFHLKGIDLDLQTHSRELPCVYFQNTIIFDNKAHSGKIKIY 264
QY 275 LETQAHIOECKHPSPVFOHGDS--FRLFDVVVILTCSLSFLLCARSLRGFLQLQNEFVG 332
DB 265 FSDAKIECKDLNIEFGSAQKQKQYVLFDAFVIVCLASLICTRSIVLALRLKRFNLN 324
QY 333 FMRQRGRVISLWLEFVNGWYILVATSDVLTISGTIMKIGIEAKNLASYDVCSILLGT 392
DB 325 FFELEKRPVCDTDQWFEFNGWVLIISDLMTIIGSILKMEIKAKNLTYDLCISFLGT 384
QY 393 STLLVWGVIRVLTFFHNNIILATLRLVPSVPMRCCCVAVIYGYCGGNTVLGPYHV 452
DB 385 STLLVWGVIRVLTFFHNNIILATLRLVPSVPMRCCCVAVIYGYCGGNTVLGPYHV 444
QY 453 KFRSLMSVSECLFSLINGDDMFVTFAAMAOQGRSLWLFSLQVLYSFLSIYVNLST 512
DB 445 KFNELNTVAECLFSLVNGDDMFATFA--QIQQ-KSILWLFSLRSLYLSIFSLIYVNLST 501
QY 513 FIALITGAYDTTIKHPGGAESEIQAQYIAQODSPTSGKFRRGSGSACSLCCGCCDRPS 572
DB 502 FIALITSDYDTTIKTPQNGFPETDLQEFLEKCS---SKEEYQKSSAFSLSCICRRKRKS 558
QY 573 EHSLLVN 580
DB 559 DDHLIPIS 566

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RESULT 9
ABU12052
ID   ABU12052 standard; Protein; 544 AA.
XX

```

AC ABU12052;
 XX
 DT 19-FEB-2003 (first entry)
 XX
 DE Human NOV9b CG90709-02 protein SEQ ID 24.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaeamic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200281625-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US10366.
 XX
 PR 03-APR-2003; 2001US-281086P.
 PR 05-APR-2003; 2001US-281306P.
 PR 06-APR-2003; 2001US-282020P.
 PR 10-APR-2003; 2001US-282930P.
 PR 12-APR-2003; 2001US-283444P.
 PR 12-APR-2003; 2001US-283512P.
 PR 13-APR-2003; 2001US-283657P.
 PR 13-APR-2003; 2001US-283678P.
 PR 13-APR-2003; 2001US-283710P.
 PR 17-APR-2003; 2001US-284234P.
 PR 19-APR-2003; 2001US-285325P.
 PR 20-APR-2003; 2001US-285381P.
 PR 24-APR-2003; 2001US-286068P.
 PR 25-APR-2003; 2001US-286292P.
 PR 07-JUN-2003; 2001US-296692P.
 PR 26-JUN-2003; 2001US-300883P.
 PR 08-AUG-2003; 2001US-311003P.
 PR 13-AUG-2003; 2001US-311973P.
 PR 16-AUG-2003; 2001US-312901P.
 PR 14-SEP-2003; 2001US-322283P.
 PR 05-OCT-2003; 2001US-327448P.
 PR 31-DEC-2003; 2001US-345734P.
 PR 03-JAN-2004; 2002US-345755P.
 PR 04-FEB-2004; 2002US-354351P.
 PR 02-APR-2004; 2002US-0114153.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson G;
 PI Guo X, Gerlach V, Gasman SJ, Boldog FL, Li L, Zerhusen BD;
 PI Tchernev VT, Gangolli EA, Vernet CM, Spytek KA, Malyankar UM;
 PI Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA;
 PI Catterton E, MacDougall JR, Edinger SR, Stone DJ, Mazur A;
 XX
 WIPI; 2003-046862/04.
 DR N-PSDB; ABX56272.
 DR
 XX New isolated NOVX polypeptide useful for treating cardiomyopathy,
 PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
 PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
 PT cancer.
 XX
 PS Claim 1; Page 111; 425pp; English.
 XX
 CC This invention describes novel polypeptides, termed NOVX which have
 CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
 CC neuroprotective, antiparkinsonian, antilipaeamic, cytostatic, nootropic,
 CC cardiant and immunomodulatory activity. The polypeptide and any
 CC antibodies generated from it are useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease
 CC selected from a pathology associated with the NOVX polypeptide. Fragments

CC and portions of the polynucleotides encoding NOVX polypeptides are useful
 CC to map the location of NOVX genes on a chromosome, to identify
 CC individuals from minute biological samples, as DNA markers for
 CC restriction fragment length polymorphism (RFLP), and are useful to
 CC prepare polymerase chain reaction primers. The products of the invention
 CC can be used in gene therapy and for treating cardiomyopathy, metabolic
 CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
 CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
 CC disease, immune disorders, haematopoietic disorders, and various
 CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
 CC syndrome X and wasting disorders associated with chronic diseases and
 CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
 CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306.
 XX
 SQ Sequence 544 AA;
 Query Match 44.6%; Score 1367; DB 24; Length 544;
 Best Local Similarity 49.2%; Pred. No. 1.9e-138;
 Matches 269; Conservative 112; Mismatches 144; Indels 22; Gaps 8;
 Qy 37 BEEDLRRLKYPFMSPCDKFRAGRKPKXLMQVVKLVVTVQLILFGLSNQLAVTFREE 96
 Db 9 KEECLREDLKFEVMSPEKRYRARRQIPWKLQILKIVMTTQLVRFGLSNQLVAFKED 68
 Qy 97 NTIAFRHLFLGYSQDADTF--AAYTRELQYCAIFHAVDOYVALPDYSLGRYAYVRGG 154
 Db 69 NTVAFKHLFLKGYSGTDEDDYSCSVYQEDAYESIFFAINQYHQLKDIITGLGY---G 124
 Qy 155 DPWTNGSLGALCORYYHGRHVPANDTFIDIMWVTDCIQVDPPEPPPPPPDDLTLLPS 214
 Db 125 ENEDNRIGLKVKCKQHYKGTGTFPSNETLINDVELDCVQLDLQDLKKPPD----WKN 179
 Qy 215 SSSYKMLTKFKHLNVVTHFRKLTINLOSINNEIPDCYTSVLITFDNKAHSGRIPIS 274
 Db 180 SSFPR---LEFYELQVEISFHLKIDLTQTHSRELPCYVFQNTIIFDNKAHSGKIKY 236
 Qy 275 LETOAHIQECKSPSVFQHGDN--FELLDFVWVILTCSLSFLLCARSLRGLLQNEFYG 332
 Db 237 FDSDAKIECKDLNIPGSAQKNAQYVDFDAFVIVCLASLILCTFSIVLALRLKRFNL 296
 Qy 333 FWRQRGRVISLWERLEFVNGWYILVTSVLTIGTITMKIGIEAKNLASVYVCSILLGT 392
 Db 297 FFLEKYKRPVCDTDQWEFNGWYVLIISDLMTIIGSILKMEIKAKNLNYDLCSIFLGT 356
 Qy 393 STLLVWGVIRYLTFPHNYNLIATLVALPSVMRECCVAVIYLGVCFCGWIILGPHV 452
 Db 357 STLLVWGVIRYLGYPQAINVILTHQASLPKVLRFACAGWIYLGTYTCGIVLGPYHD 416
 Qy 453 KFRSLNWSCELSFLINGDDMFVTFAMQAQQGRSLVMSFLSOLYLYSIFSIYVMSLS 512
 Db 417 KPENLNTVABCLFSLVNGDDMPATFA--QIQQ-KSILVMSFLSRLYLSIFSIYVMSLS 473
 Qy 513 FIALLTGANDTIKHPGAGASELQAYIAQQODSPSGKPRGSGSACSLCCCGDPS 572
 Db 474 FIALLTDSYDTIKKFOONGFPETDLQELKECS---SKEEYOKESAFUSLCCRRRSVS 530
 Qy 573 EEHSLIV 579
 Db 531 CLFSMLL 537
 RESULT 10
 ABU12051
 ID ABU12051 standard; Protein; 540 AA.
 AC ABU12051;
 XX
 DT 19-FEB-2003 (first entry)
 XX
 DE Human NOV9a CG90709-01 protein SEQ ID 22.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;

PF 24-MAY-2001; 2001WO-NZ00099.
 XX
 PR 24-MAY-2000; 2000US-206650P.
 PR 25-JUL-2000; 2000US-221232P.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
 PI WPI; 2002-122020/16.
 DR N-PSDB; ABL35079.
 XX
 XX New polynucleotides and polypeptides encoded by the polynucleotides
 PT isolated from skin cells, useful for treating skin wounds, cancers,
 PT growth and developmental defects, inflammatory diseases, or for
 PT modulating immune responses -
 XX
 XX Claim 4; Page 455; 466pp; English.
 PS
 CC The present invention provides the protein and coding sequences of cDNAs
 CC isolated from human, murine and rat skin cell libraries. The sequences
 CC can be used in the development of therapeutic agents useful in the
 CC treatment of skin diseases, including skin wounds, cancer, growth
 CC defects, developmental defects and inflammatory diseases. The proteins
 CC have important roles in the induction of hair growth, cell proliferation
 CC and cell-cell interaction, in maintaining tissue integrity, in wound
 CC healing and in modulating immune responses. The present sequence is a
 CC polypeptide of the invention.
 XX
 XX Sequence 255 AA;
 SQ
 Query Match 40.0%; Score 1226; DB 23; Length 255;
 Best Local Similarity 89.7%; Pred. No. 1.1e-123;
 Matches 227; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
 QY 37 EEDLRRRLKYYFMSPCDKFRAGKRPCKMLQVVKILVTVQLILFGLSNQLAVTFREE 96
 Db 1 EEDLRRRLKYYFMSPCDKFRAGKRPCKMLQVVKILVTVQLILFGLSNQLAVTFREE 60
 QY 97 NTIAFRHLFLGYSDGADTFAAATREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDP 156
 Db 61 NTIAFRHLFLGYSDGDDTFAATYQEQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDP 120
 QY 157 WTNGSLALCQYYHGHVDPANDTFDIDPMVVTDCIQVDPPEPPPSDDLTLESS 216
 Db 121 WANGSALALCQYYHGHVDPANDTFDIDPMVVTDCIQVDPPEPPPSDDLTLESS 180
 QY 217 SYKNLTLPKHLVNTIHFRLKTNILQSLINNEIPDCYTFSLITFDNKAHSGRIPI 276
 Db 181 SYKNLTLPKHLVNTIHFRLKTNILQSLINNEIPDCYTFSLITFDNKAHSGRIPI 240
 QY 277 TQAHQCEKHPSV 289
 Db 241 TKTHIQCEKHPSV 253
 RESULT 12
 ID ABB71675
 XX ABB71675 standard; Protein; 652 AA.
 AC ABB71675;
 XX
 XX 26-MAR-2002 (first entry)
 DT Drosophila melanogaster polypeptide SEQ ID NO 41817.
 DE Drosophila melanogaster polypeptide; cell signalling; insecticide;
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 FN
 XX

PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656960/75.
 DR N-PSDB; ABL15778.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX Disclosure; SEQ ID NO 41817; 21pp + Sequence Listing; English.
 PS
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 652 AA;
 SQ
 Query Match 33.4%; Score 1025.5; DB 22; Length 652;
 Best Local Similarity 37.3%; Pred. No. 2.4e-101;
 Matches 233; Conservative 119; Mismatches 190; Indels 83; Gaps 19;
 QY 2 TAPAGRGSETERLLTPNPGYGTQAGSPAPPT-----PPE-----EEDLRRRL 45
 Db 51 STVPAP-----VVMP-----ISAGSTAPPVSDGREEQEPFGSSAASYQERNRKL 99
 QY 46 KYFMSPCDKFRAGKRPCKMLQVVKILVTVQLILFGLSNQLAVTFREENTIAFRHL 105
 Db 100 QFFEMPIEKQAKRPFPYVQVIVFLVTVQLILFGLSNQLAVTFREENTIAFRHL 159
 QY 106 LLGYSDG-----ADDTFAAYTREQLYQAIHFAVDQYLALPDVSLGRYAYVRGGDP 157
 Db 160 LRGWSSREVESYPPAVGPFALYKSEFDTQVAVNGY-ANVRSIGFYD-----PT 212
 QY 158 TNGS--GLALCQYYHGHVDPANDTFDIDPMVVTDCIQVDPPEPPPSDDLTLL--E 213
 Db 213 PNNTMPPLKCLQNYREGTIFGNESYIFDPHIDEVC-----ERLPP-----NVTIGVE 262
 QY 214 SSSSYKNLTLPKHLVNTIHFRLKTNILQSLINNEIPDCYTFSLITFDNKAHSGR 270
 Db 263 NYLRQDVEVNFASLYSAQLTFKIKTVNPKA--NGGPLSAPDCFRFDISITFNDRHDOQ 320
 QY 271 IPISLETQAHIOECKHPSV--OHGDNFRLLFDVVVILTCSLFPLLCARSLRGLFLO 327
 Db 321 MLISLDAEATRLKCHGATDFISDANFDSMLRSVLNIFVLLTCALSFALCTRALWYLLR 380
 QY 328 NERVGFMRQRGRVISLWERLRFVNGVILLVTSVLTISGTIMKIGIEAKLA--SYDV 385
 Db 381 CTTVNFRSFGKELSDGRLEFVNFWYIMIFNDVLLIIGSALKKEQIEGRVILVDQWDT 440
 QY 386 CSILGTSTLLVWVGVIYRLTFPHNYNIIATLRVALPSWFRFCVAVIYLYGFCGWI 445
 Db 441 CSLFLGIGNLLVWVGVIYRLTFPHNYNIIATLRVALPSWFRFCVAVIYLYGFCGWI 500
 QY 446 VLPYHVKFRSLSMWSECLFSLINGDDMFVTFAMQAQQGRSSLVWLPFQLYLSPISLF 505
 Db 501 ILGPHYHMKFRSLATTSECLFALINGDDMFATLSS---KATWLWVFCQIYLYSPISLY 557

QY 506 IYVLSLFIALLITGAYDTIKHFGGAGAESELOAVI-AQCQDSPTSGKF-----RRG 556
 Db 558 IYVLSLFIPIAVIMDAYDTIKAYYKDGFTTDLKAFVGTARTAEISSGVFMTDLDDFOQTS 617
 QY 557 SGSACSLCCCGR-----DPSEHS 576
 Db 618 FLDVVKSICCCGRCGRHQPAPNS 642

RESULT 13
 ABG01744
 ID ABG01744 standard; Protein; 191 AA.
 AC ABG01744;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #1735.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS65931.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 32103; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 191 AA;
 Query Match 31.9%; Score 979; DB 22; Length 191;

Best Local Similarity 98.4%; Pred. No. 3.9e-97;
 Matches 183; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MTAPAGRGSETERLLTFNPGYGTQAGSPAPPTPPPEEDLRRRLKYFFMSPCDKFRAG 60
 Db 1 MTAPAGRGSETERLLTFNPGYGTQAGSPAPPTPPPEEDLRRRLKYFFMSPCDKFRAG 60
 QY 61 RKPKMLQVVKILVVTQVQLILFGLSNQLAVTFRENTIAFRHLFLGLYSGADDTFAAY 120
 Db 61 RKPKMLQVVKILVVTQVQLILFGLSNQLAVTFRENTIAFRHLFLGLYSGADDTFAAY 120
 QY 121 TREOLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSLGALCORYYHRGHVDPAND 180
 Db 121 TREOLYQAIHFAVDQYLALPDVSLGRYAYVRGGDPWTNGSLGALCORYYHRGHVDPAND 180
 QY 181 TFDIDP 186
 Db 181 TFDIDP 186

RESULT 14
 AAU00503
 ID AAU00503 standard; Protein; 193 AA.
 XX
 AC AAU00503;
 XX
 DT 18-JUL-2001 (first entry)
 XX
 DE Human TANGO 480 protein.
 XX
 KW Human; TANGO 315; clone jthkal73a09; TANGO 330; TANGO 437; TANGO 480;
 KW cellular process regulator; gene therapy; keratinocyte disorder;
 KW squamous cell carcinoma; keratitis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
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 FT /label= Signal_peptide
 FT Misc-difference 3
 FT /note= "Alternatively this residue is Val due to
 FT species variation"
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 PN WO200123523-A2.

neurological disease; infection; human; secreted protein.

Homo sapiens.

WO200190304-A2.

29-NOV-2001.

18-MAY-2001; 2001WO-US16450.

19-MAY-2000; 2000US-205515P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

WPI; 2002-122018/16.

N-PSDB; ABL89699.

Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, PT Gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders - PT

Claim 11; SEQ ID NO 1666; 2081pp + Sequence Listing: English.

The invention relates to novel genes (ABL89449-ABL90853) and proteins (AB89040-AB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune; (c) haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (d) cardiovascular disorders such as myocardial ischaemias; (e) wound healing; (f) neurological diseases e.g. cerebral anoxia and epilepsy; and (g) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 154 AA;

Query Match 20.4%; Score 627; DB 23; Length 154;

Best Local Similarity 98.3%; Pred. No. 3.7e-59;

Matches 118; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MWRQGRVTSLWERLFVNGWILLTSDVLTISGTIMKIGIEAKNLASYDVCISLLGTS 60

QY 394 TLLVWVGVIYLTFFHNYNILLATLVALPSVNRFCCECCVAVIYLGVCFCGWIYLPVHVK 453

Db 61 TLLVWVGVIYLTFFHNYNILLATLVALPSVNRFCCECCVAVIYLGVCFCGWIYLPVHVK 120

Search completed: October 27, 2003, 18:03:49

Job time : 97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Total number of hits satisfying chosen parameters: 3584790
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2	1101	100.0	1740	13	US-10-103-458-3	Sequence 3, Appli
3	1101	100.0	2095	9	US-09-828-466-1	Sequence 1, Appli
4	1101	100.0	2095	13	US-10-103-458-1	Sequence 1, Appli
5	1100.2	99.9	2094	9	US-09-820-893-26	Sequence 26, Appl
6	1099.4	99.9	2052	10	US-09-965-529-50	Sequence 50, Appl
7	1099.4	99.9	2052	11	US-09-969-680A-50	Sequence 50, Appl
8	851.4	77.3	1827	11	US-09-866-050A-608	Sequence 608, App
9	851.4	77.3	1827	14	US-10-152-661-608	Sequence 608, App
10	203.8	18.5	1912	11	US-09-796-753-161	Sequence 161, App
11	199.8	18.1	1671	12	US-10-114-153-23	Sequence 23, Appl
12	199.8	18.1	2067	12	US-10-114-153-27	Sequence 27, Appl
13	199.8	18.1	2130	12	US-10-114-153-25	Sequence 25, Appl
14	183.8	16.7	1677	12	US-10-305-810-4	Sequence 4, Appli
15	183.8	16.7	1677	12	US-10-114-153-21	Sequence 21, Appl
16	56	5.1	720	13	US-10-101-487-74	Sequence 74, Appl

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18	51.8	4.7	1125	14	US-10-156-761-7230	Sequence 7230, Ap
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21	49.6	4.5	520	14	US-10-184-634-332	Sequence 332, App
22	49.2	4.5	554	13	US-10-101-487-106	Sequence 106, App
23	49.2	4.5	783	12	US-09-953-348-99	Sequence 99, Appl
24	49.2	4.5	783	14	US-10-267-255-99	Sequence 99, Appl
25	49.2	4.5	3765	12	US-09-953-348-9	Sequence 9, Appli
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ALIGNMENTS

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; Sequence 3, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: Silos-Santiago, Immaculada
; FILE REFERENCE: WNI-125CP
; CURRENT APPLICATION NUMBER: US/09/828,466
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/544,797
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1740)
US-09-828-466-3

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; Sequence 3, Application US/10103458
; Publication No. US20020197680A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
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; FILE REFERENCE: MNI-125
; CURRENT APPLICATION NUMBER: US/10/103,458
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US/09/544,797
; PRIOR FILING DATE: PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1740)
US-10-103-458-3
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Best Local Similarity 100.0%; Pred. No. 11e-298; Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (141)..(1880)
US-10-103-458-1

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Best Local Similarity 100.0%; Pred. No. 1.2e-298;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 CCATCCACTCCGGCTGAAGACCATTAACCTCAGAGCTTCATCAATATGAGATCCCGG 480
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DB 895 ACTGCTATACCTTCAGGCTCCTGATCAGCTTTGACAAACAAAGCACAGTGGCGGATCC 954

QY 541 CCATCAGCTGGAGACCCAGGCCCAATCCAGAGTGTAAAGCAGCTGCTTCCAGC 600
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; Sequence 26, Application US/09820893
; Patent No. US20020076705A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human Secreted Proteins
; FILE REFERENCE: P2033P1
; CURRENT APPLICATION NUMBER: US/09/820,893
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/102,895
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2078)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-820-893-26
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Query Match      99.9%; Score 1100.2; DB 9; Length 2094;
Best Local Similarity 99.8%; Pred. No. 2e-298;
Matches 1099; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCGGGAGAGAACACCATCGCTTCGGACACCTCTCTCTGGGCTACTCGGACG 60
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QY 61 GAGGGATGACACCTTCGAGCCTACACGGGGAGAGAGCTGTACCGCCCATCTTCATG 120
DB 442 GAGGGATGACACCTTCGAGCCTACACGGGGAGAGAGCTGTACCGCCCATCTTCATG 501

QY 121 CTGTGACCACTACCTGGGCTTCGCTGCTGCTGCGCGGTATGCTATGCTCGG 180
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QY 181 GTGGGGGTGACCTTCGAGCAATGCTCAGGCTTCGCTCTGCGAGCGGTACTACCA 240
DB 562 GTGGGGGTGACCTTCGAGCAATGCTCAGGCTTCGCTCTGCGAGCGGTACTACCA 621

QY 241 GAGGCCAGTGGACCGCGCCAAACACATTTGACATTTGATTCGATGGTGTACTGACT 300
DB 622 GAGGCCAGTGGACCGCGCCAAACACATTTGACATTTGATTCGATGGTGTACTGACT 681

QY 301 GCATCAGGTGGATCCCGCGAGCGGCCCTCGCGCCCGCGAGCTCAACCTCTCAGCCTCT 360
DB 682 GCATCAGGTGGATCCCGCGAGCGGCCCTCGCGCCCGCGAGCTCAACCTCTCAGCCTCT 741

QY 361 TGAAGAGAGCTTCAGTTTACAGAACCTCAAGCTCAAAATTCACAGCTGGTCAATGTCA 420
DB 742 TGAAGAGAGCTTCAGTTTACAGAACCTCAAGCTCAAAATTCACAGCTGGTCAATGTCA 801

QY 421 CCATCCACTTCGCGCTGAAGACCATTAACCTCCAGAGCTTCATCAATATGAGATCCCGG 480
```

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Db      802  CCAATCCACTCCGGCTGAGACCACTTACCTCCAGAGCTCATCAATATGAGATCCCGG 861
Qy      481  ACTGCTATACCTTCAGGCTCCTGATACGTTTGAACAACAAAGCACACAGTGGGGATCC 540
Db      862  ACTGCTATACCTTCAGGCTCCTGATCAGTTTGACAAACAAAGCACACAGTGGGGATCC 921
Qy      541  CCATCAGCTGGAGACCCAGCCACATCCAGAGGTGAAGACCCCAAGTCTTCCAGC 600
Db      922  CCATCAGCTGGAGACCCAGCCACATCCAGAGGTGAAGACCCCAAGTCTTCCAGC 981
Qy      601  ACGGAGACAAAGCTTCGGGCTCCTGTTTGACGTTGGTGTCTCATCTCACCCTGCTCCCTGT 660
Db      982  ACGGAGACAAAGCTTCGGGCTCCTGTTTGACGTTGGTGTCTCATCTCACCCTGCTCCCTGT 1041
Qy      661  CTTTCTCTCTCTGGCCCGCTCATCTCTTCAGAGGTTCTCTCTGACAGAACAGTTTGTGG 720
Db      1042  CTTTCTCTCTCTGGCCCGCTCATCTCTTCAGAGGTTCTCTCTGACAGAACAGTTTGTGG 1101
Qy      721  GGTTCATGTGGCGCAGCGGAGCGGTTCATCAGCCTGTGGAGCGCTGGAATTTGTCA 780
Db      1102  GGTTCATGTGGCGCAGCGGAGCGGTTCATCAGCCTGTGGAGCGCTGGAATTTGTCA 1161
Qy      781  ATGCTCGTATACCTCTGCTGCTACCAAGCGATGTGCTCACCATCTCGGGCACCATATGA 840
Db      1162  ATGCTCGTATACCTCTGCTGCTACCAAGCGATGTGCTCACCATCTCGGGCACCATATGA 1221
Qy      841  AGATCGCATCGAGGCCAAGAACTTGGGAGCTAGAGCTGTGAGATCTCTCTCTGGGCA 900
Db      1222  AGATCGCATCGAGGCCAAGAACTTGGGAGCTAGAGCTGTGAGATCTCTCTCTGGGCA 1281
Qy      901  CCTCGAGCTGTGCTGTGGTGGGCTGATCCGCTACCTACCTGATCTCTCCACAACTACA 960
Db      1282  CCTCGAGCTGTGCTGTGGTGGGCTGATCCGCTACCTACCTGATCTCTCTCCACAACTACA 1341
Qy      961  ATATCTCATGCGCACACTCGGCTGGCCCTGCCAGCGTCAATCGGTTCTGTGCTGGC 1020
Db      1342  ATATCTCATGCGCACACTCGGCTGGCCCTGCCAGCGTCAATCGGTTCTGTGCTGGC 1401
Qy      1021  TGGCTGTCACTACTGCGCTACTGCTTCTGTGCTGATGCTGCTGGGCGCTTATCATG 1080
Db      1402  TGGCTGTCACTACTGCGCTACTGCTTCTGTGCTGATGCTGCTGGGCGCTTATCATG 1461
Qy      1081  TGAAGTTCCGCTCACTCTCCA 1101
Db      1462  TGAAGTTCCGCTCACTCTCCA 1482
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RESULT 6

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US-09-965-529-50
; Sequence 50, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731 USA
; CURRENT APPLICATION NUMBER: US/09965529
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315
; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 50
; LENGTH: 2052
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 977658CB1
US-09-965-529-50
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Query Match      99.9%; Score 1099.4; DB 10; Length 2052;
Best Local Similarity 99.9%; Pred. No. 3.4e-298;
Matches 1100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1  CATTCCGGGAGAGAACACCATCGCTTCGACACCTTCTCCCTGCTGGGCTACTCGGAGC 60
Db      382  CATTCCGGGAGAGAACACCATCGCTTCGACACCTTCTCCCTGCTGGGCTACTCGGAGC 441
Qy      61  GAGCGGATGACACTTCGAGCCTTACACGCGGGAGCAGCTGTACACGGCCATCTTCCATG 120
Db      442  GAGCGGATGACACTTCGAGCCTTACACGCGGGAGCAGCTGTACACGGCCATCTTCCATG 501
Qy      121  CTGTGGACCACTACCTGGCGTTGCTGACGTGTACCTGAGCCGCTATGCGGTATGCTCGTG 180
Db      502  CTGTGGACCACTACCTGGCGTTGCTGACGTGTACCTGAGCCGCTATGCGGTATGCTCGTG 561
Qy      181  GTGGGGGTGACCTTGGACCAATGGCTTCAGGCTTGTCTCTGCGACGGGTACTACCAACC 240
Db      562  GTGGGGGTGACCTTGGACCAATGGCTTCAGGCTTGTCTCTGCGACGGGTACTACCAACC 621
Qy      241  GAGGCCACGTGGACCCCGGCCAACACACATTTGACATTTGATTCGATGGTGTACTGACT 300
Db      622  GAGGCCACGTGGACCCCGGCCAACACACATTTGACATTTGATTCGATGGTGTACTGACT 681
Qy      301  GCATCCAGGTGGATCCCCCGGAGCGGCCCTCGGCCCGCCAGGACGATCTCAACCTCT 360
Db      682  GCATCCAGGTGGATCCCCCGGAGCGGCCCTCGGCCCGCCAGGACGATCTCAACCTCT 741
Qy      361  TGGAAAGCAGCTCCAGTTTAAAGAACCTCAGCTCAAAATTCACAAAGCTGTGTAATGTCA 420
Db      742  TGGAAAGCAGCTCCAGTTTAAAGAACCTCAGCTCAAAATTCACAAAGCTGTGTAATGTCA 801
Qy      421  CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAGATGCCCGG 480
Db      802  CCATCCACTTCCGGCTGAAGACCATTAACCTCCAGAGCCTCATCAATAGATGCCCGG 861
Qy      481  ACTGCTATACCTTCAGGCTCCTGATCAGCTTTGACAAAGCACACAGTGGGGGATCC 540
Db      862  ACTGCTATACCTTCAGGCTCCTGATCAGCTTTGACAAAGCACACAGTGGGGGATCC 921
Qy      541  CCATCAGCTGGAGACCCAGGCCACATCCAGAGGTGAAGACCCCAAGTGTCTTCCAGC 600
Db      922  CCATCAGCTGGAGACCCAGGCCACATCCAGAGGTGAAGACCCCAAGTGTCTTCCAGC 981
Qy      601  ACGGAGACAAAGCTTCGGGCTCCTGTTTGAAGTGTGTTGCTCCTCACCCTGCTCCCTGT 660
Db      982  ACGGAGACAAAGCTTCGGGCTCCTGTTTGAAGTGTGTTGCTCCTCACCCTGCTCCCTGT 1041
Qy      661  CTTTCTCTCTCTGGCCCGCTCACTCTCTGAGGCTTCTGCTGACAGAACAGTTTGTGG 720
Db      1042  CTTTCTCTCTCTGGCCCGCTCACTCTCTGAGGCTTCTGCTGACAGAACAGTTTGTGG 1101
Qy      721  GGTTCATGTGGCGCAGCGGAGCGGTTCATCAGCCTGTGGAGCGCTGGAATTTGTCA 780
Db      1102  GGTTCATGTGGCGCAGCGGAGCGGTTCATCAGCCTGTGGAGCGCTGGAATTTGTCA 1161
Qy      781  ATGCTCGTATACCTCTGCTGCTCACCAGCGATGTGCTCACCATCTCGGGCACCATATGA 840
Db      1162  ATGCTCGTATACCTCTGCTGCTCACCAGCGATGTGCTCACCATCTCGGGCACCATATGA 1221
Qy      841  AGATCGCATCGAGGCCAAGAACTTGGGAGCTAGAGCTGTGAGATCTCTCTCTGGGCA 900
Db      1222  AGATCGCATCGAGGCCAAGAACTTGGGAGCTAGAGCTGTGAGATCTCTCTCTGGGCA 1281
Qy      901  CCTCGAGCTGTGCTGTGGTGGGCTGATCCGCTACCTACCTGATCTCTCTCCACAACTACA 960
Db      1282  CCTCGAGCTGTGCTGTGGTGGGCTGATCCGCTACCTACCTGATCTCTCTCTCCACAACTACA 1341
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QY 961 ATATCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCAATGCGCTTCTGCTCTGG 1020
 DB 1342 ATATCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCAATGCGCTTCTGCTCTGG 1401
 QY 1021 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATG 1080
 DB 1402 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATG 1461
 QY 1081 TGAAGTTCCGCTCACTCTCCA 1101
 DB 1462 TGAAGTTCCGCTCACTCTCCA 1482

RESULT 7

US-09-969-680A-50
 ; Sequence 50, Application US/09969680A
 ; Publication No. US20030124649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAL, Preeti; YUE, Henry
 ; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
 ; APPLICANT: BURFORD, Neil; AZIMZAI, Yalda
 ; APPLICANT: BAUGHN, Mariah R.; LU, Dying Aina M.
 ; APPLICANT: PATTERSON, Chandra
 ; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0731-1 USA
 ; CURRENT APPLICATION NUMBER: US/09/969,680A
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US00/22315
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/149,641
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/164,203
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 50
 ; LENGTH: 2052
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20030124649A1 977658CB1
 US-09-969-680A-50

Query Match 99.9%; Score 1099.4; DB 11; Length 2052;
 Best Local Similarity 99.9%; Pred. No. 3.4e-298;

Matches 1100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATTCGGGAAGAGAACACCATCGCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 60
 DB 382 CATTCGGGAAGAGAACACCATCGCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG 441
 QY 61 GAGCGGATGACACCTTCCGACCTACAGCGGGAGAGCTGTACAGGCCATCTTCCATG 120
 DB 442 GAGCGGATGACACCTTCCGACCTACAGCGGGAGAGCTGTACAGGCCATCTTCCATG 501
 QY 121 CTGTGGACCACTACTGCGGCTTGTCTGACGCTGCTACGCGCGGTATCGGTATCGCGTG 180
 DB 502 CTGTGGACCACTACTGCGGCTTGTCTGACGCTGCTACGCGCGGTATCGGTATCGCGTG 561
 QY 181 GTGGGGGTGACCTTGGACCAATGGCTCAGGGCTTGTCTCTGCGAGCGGTACTACCAACC 240
 DB 562 GTGGGGGTGACCTTGGACCAATGGCTCAGGGCTTGTCTCTGCGAGCGGTACTACCAACC 621
 QY 241 GAGGCCAGTGAGCCCGCCCAACACACATTGACATGATCCGATGTTGTTACTGACT 300
 DB 622 GAGGCCAGTGAGCCCGCCCAACACACATTGACATGATCCGATGTTGTTACTGACT 681
 QY 301 GCATCCAGGTGATCCCGCGGCGCCCTCCGCCCCCAGCGAGATCTCAACCTCT 360
 DB 682 GCATCCAGGTGATCCCGCGGCGCCCTCCGCCCCCAGCGAGATCTCAACCTCT 741

QY 361 TGGAAAGCAGCTCCAGTTAGACACCTCAGCTCAATTTCCACAGCTGCTCAATGTCA 420
 DB 742 TGGAAAGCAGCTCCAGTTAGACACCTCAGCTCAATTTCCACAGCTGCTCAATGTCA 801
 QY 421 CCATCCACTTCCGGCTGAAGACCAATTAACTCCAGAGCTTCATCAATAATGAGATCCCGG 480
 DB 802 CCATCCACTTCCGGCTGAAGACCAATTAACTCCAGAGCTTCATCAATAATGAGATCCCGG 861
 QY 481 ACTGCTATACCTTCAAGCTTCTGATCAGCTTTTGAACAACAAAGCACACAGTGGGGGATCC 540
 DB 862 ACTGCTATACCTTCAAGCTTCTGATCAGCTTTTGAACAACAAAGCACACAGTGGGGGATCC 921
 QY 541 CCATCAGCTGGAGACCCAGCCCCACATCCAGGAGTGTAAAGCACCCAGTGTCTTCCAGC 600
 DB 922 CCATCAGCTGGAGACCCAGCCCCACATCCAGGAGTGTAAAGCACCCAGTGTCTTCCAGC 981
 QY 601 ACGGAGACACAGCTTCCGGCTCTCTTTTGAAGTGTGCTCATCTCACTCTCCCTGT 660
 DB 982 ACGGAGACACAGCTTCCGGCTCTCTTTTGAAGTGTGCTCATCTCACTCTCCCTGT 1041
 QY 661 CTTTCTCTCTTGGCGCCGCTCACTCTTGGAGCTTCTGCTGAGAACAGAGTTTGG 720
 DB 1042 CTTTCTCTCTTGGCGCCGCTCACTCTTGGAGCTTCTGCTGAGAACAGAGTTTGG 1101
 QY 721 GGTTCATGTGGCGCAGCGGAGCGGCTCATCAGCTGTGGAGCGGCTGGAATTTGTCA 780
 DB 1102 GGTTCATGTGGCGCAGCGGAGCGGCTCATCAGCTGTGGAGCGGCTGGAATTTGTCA 1161
 QY 781 ATGCTGTGTATACCTCTCTCTCACCAGCATGTGCTCACCATCTCGGGACCATCATGA 840
 DB 1162 ATGCTGTGTATACCTCTCTCTCACCAGCATGTGCTCACCATCTCGGGACCATCATGA 1221
 QY 841 AGATCGGCATCGAGGCCAAGAACTTGGCAGCTACGACGTCTGAGCATCTCTCTGGSCA 900
 DB 1222 AGATCGGCATCGAGGCCAAGAACTTGGCAGCTACGACGTCTGAGCATCTCTCTGGSCA 1281
 QY 901 CCTCGACGTGCTGTGGTGGGCGTGATCCGCTACCTGACCTTCTTCCACAACTACA 960
 DB 1282 CCTCGACGTGCTGTGGTGGGCGTGATCCGCTACCTGACCTTCTTCCACAACTACA 1341
 QY 961 ATATCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCAATGCGCTTCTGCTGCTGCG 1020
 DB 1342 ATATCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTCAATGCGCTTCTGCTGCTGCG 1401
 QY 1021 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATG 1080
 DB 1402 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGGCTGGATCGTCTGGGGCCCTATCATG 1461
 QY 1081 TGAAGTTCCGCTCACTCTCCA 1101
 DB 1462 TGAAGTTCCGCTCACTCTCCA 1482

RESULT 8

US-09-866-050A-608
 ; Sequence 608, Application US/09866050A
 ; Publication No. US20030040471A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Marison, James G.
 ; APPLICANT: Kumbie, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; TITLE OF INVENTION: and Methods for Their Use
 ; FILE REFERENCE: 11000.1011c4U
 ; CURRENT APPLICATION NUMBER: US/09/866,050A
 ; CURRENT FILING DATE: 2001-05-24
 ; NUMBER OF SEQ ID NOS: 725
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 608
 ; LENGTH: 1827

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i TYPE: DNA
; ORGANISM: Mouse
US-09-866-050A-608

Query Match      77.3%; Score 851.4; DB 11; Length 1827;
Best Local Similarity 85.8%; Pred. No. 1.2e-228;
Matches 945; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

Qy 1 CATTCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCCTGCTGGGCTACTCGGACG 60
Db 167 CATTCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCCTGCTGGGCTACTCTGATG 226

Qy 61 GAGCGGATGACACCTTCGACCTTACAGCGGGAGCAGCTGACAGGCCATCTCCATG 120
Db 227 GGTCTGATGACACCTTTGACGCTTACACAGGAGCAGCTCTACCAAGCCATCTTCTATG 286

Qy 121 CTGTGGACCACTGACCTTCGACCTTCCTGACCTGCTGAGGCGGTATGCGTATGTCGGTG 180
Db 287 CTGTGGACCACTGACCTTCGACCTTCCTGACCTGCTGAGGCGGTATGCGTATGTCGGTG 346

Qy 181 GTGGGGGTGACCTTCGACCAATGGCTCAGGCTTCTCTGCGACGGGTACTACCAACC 240
Db 347 GTGGGGGTGACCTTCGACCAATGGCTCAGGCTTCTCTGCGACGGGTACTACCAACC 406

Qy 241 GAGGCCACGTGGACCGGCCCAAGACATTTGACATTTGATCCGATGGTGTACTGACT 300
Db 407 GTGGCCATGTGGACCGGCCCAAGACATTTGACATTTGATCCGAGGTAGTCACTGACT 466

Qy 301 GCATCCAGGTGGATCCCGCCGAGCGGGCCCTCCGCCCCCGAGGAGAGATCTCAACCTCT 360
Db 467 GTATCCAGGTGGATCCCGCCGAGCGGGCCCTCCGCCCCCGAGGAGAGATCTCAACCTCT 526

Qy 361 TGGAAAGCAGCTCCAGTTACAGAACCTCAGCTCAATTCACAACTGCTCAATTCAC 420
Db 527 TGGATGCGAGCGGAGTTACAGAACCTCAGCTCAATTCACAACTGCTCAATTCAC 586

Qy 421 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCTCATCAATAGATCCCGG 480
Db 587 CCATCCACTTCCAGCTGAAGACCAATTAACCTCCAGAGCTCATCAATAGATCCCGG 646

Qy 481 ACTGCTATACCTTCAGCGTCTCTGATCAGTTTGACACAAAGCAGCAGTGGGGGATCC 540
Db 647 ATTGTTACACCTTCAGTTATCTGATCAGTTTGACAAATAGCGCAGTGGGGGATCC 706

Qy 541 CCATCAGCTGGAGACCGGCGCCACATCCAGAGGTGAAGACCCAGTGTCTTCCAGC 600
Db 707 CCATCCGCTGGAGACCGGCGCCACATCCAGAGGTGAAGACCCAGTGTCTTCCAGC 766

Qy 601 ACGGAGACACAGCTTCGCGCTCCGCTTTGAGCTGGTGTCTCATCTCAGCTGCTCCCTGT 660
Db 767 ATGGAGACACAGCTTCGCGCTTCGCTTTGATGTTGGTGTATCTTACCTGCTCCCTGT 826

Qy 661 CTTTCCTCCTCTGCGCGGCTCACTCCTTCGAGGCTTCCTGCTGCAAGAACGAGTTTGTGG 720
Db 827 CTTTCCTCCTCTGCGCGGCTCACTCCTTCGCTGCGGCTTCCTGCTGCAAGAACGAGTTTGTGG 886

Qy 721 GGTTCATGTGGCGGACGGGAGCGGTCATCAGCTGTGGAGCGGCTGGAATTCATCA 780
Db 887 TATTTCATGTGGCGGAGCGGAGTCCGGAATCAGCTTCGGAACGGCTGGAGTTTGTCA 946

Qy 781 ATGCTGTATATCTGCTGCTCAGCAGATGTGCTCAGCTATCTCCGACCATCATGA 840
Db 947 ATGCTGTATATCTGCTGCTCAGCAGATGTGCTCAGCTATCTCCGACCATCATGA 1006

Qy 841 AGATCGGCATCGAGGCCAAGAACTTGGGAGCTACGAGTCTGAGCATCTCTCTGGGCA 900
Db 1007 AGATTGGCATTTAGGCAAGAACTTGGGAGCTATGATCTGAGTATCTCTTGGGTA 1066

Qy 901 CCTCGACGCTGCTGGTGTGGGTGGCGGTATCCGCTACCTGACCTTCTTCCAACTACA 960
Db 1067 CCTCCACTCTGCTAGTCTGGGTGGGTGTCATTTGCTACTCTGACATTTTCCAACTACA 1126

Qy 961 ATATCTCTCATCGCCACACTGCGGGTGGCCCTCGCCAGGCTCATGCGCTTCTGCTGCTGGG 1020
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Db 1127 ACATCTTGATGCCACGTTGCGAGTGGCACTGCCAGTGCATCGCTTTCGCTGCTGTG 1186
Qy 1021 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGCTGGATCGTCTGGGGCCCTATCATG 1080
Db 1187 TGGCTGTCACTACCTGGGCTACTGCTTCTGTGCTGGATCGTCTTAGGGCCCTACCATG 1246
Qy 1081 TGAAGTTCGCTCACTCTCCA 1101
Db 1247 TGAAGTTCGCTCGCTGTCCA 1267

RESULT 9
US-10-152-661-608
; Sequence 608, Application US/10152661
; Publication No. US20030022835A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011cs
; CURRENT APPLICATION NUMBER: US/10/152.661
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/866,050
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/221,232
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/206,650
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/312,283
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00051
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 09/188,930
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: 09/069,726
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 608
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Mouse
US-10-152-661-608

Query Match      77.3%; Score 851.4; DB 14; Length 1827;
Best Local Similarity 85.8%; Pred. No. 1.2e-228;
Matches 945; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

Qy 1 CATTCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCCTGCTGGGCTACTCGGACG 60
Db 167 CATTCGGGAAGAGAACACCATCGCCTTCGACACCTCTTCCTGCTGGGCTACTCTGATG 226

Qy 61 GAGCGGATGACACCTTCGACCTTACAGCGGGAGCAGCTGACAGGCCATCTTCCATG 120
Db 227 GGTCTGATGACACCTTTGACGCTTACACAGGAGCAGCTCTACCAAGCCATCTTCTATG 286

Qy 121 CTGTGGACCACTGACCTTCGACCTTCCTGACCTGCTGAGGCGGTATGCGTATGTCGGTG 180
Db 287 CTGTGGACCACTGACCTTCGACCTTCCTGACCTGCTGAGGCGGTATGCGTATGTCGGTG 346

Qy 181 GTGGGGGTGACCTTCGACCAATGGCTCAGGCTTCTCTGCGACGGGTACTACCAACC 240
Db 347 GTGGGGGTGACCTTCGACCAATGGCTCAGGCTTCTCTGCGACGGGTACTACCAACC 406

Qy 241 GAGGCCACGTGGACCGGCCCAAGACATTTGACATTTGATCCGATGGTGTACTGACT 300
Db 407 GTGGCCATGTGGACCGGCCCAAGACATTTGACATTTGATCCAGGCTAGTCACTGACT 466
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QY 301 GCATCCAGTGATCCCGCCGAGCGCCCGCTCCGCCCCCAGGAGGATGTCAACCTCT 360
Db |||||
QY 467 GTATCAGGTGATCTCTCTGACAGACCCCTGACATCCCGAGTGAGGACTTCT 526
Db |||||
QY 361 TGGAAAGCAGCTCCAGTTACAAAGACCTCACGCTCAATTTCCACAGCTGGTCAATGTCA 420
Db |||||
QY 527 TGGATGGCAGCCAGTTACAAAGACCTCACACTGAATTTCCAAAGCTGATCAACGTCA 586
Db |||||
QY 421 CCATCCACTCCGGCTGAAGACCATTAACCTCCAGAGCTCATCAATATGATGATCCCGG 480
Db |||||
QY 587 CCATCCACTCCAGCTGAAGACAATTAACCTGCAGAGCTCATCAACAATGATGATCCCTG 646
Db |||||
QY 481 ACTGCTATACCTTCAGCGTCTGATCAGTTTGAAACAAAGCAACAGTGGGGGATCC 540
Db |||||
QY 647 ATTGTTACCTTCAGTATCTGATCAATTTGACAATAAAGCGACAGTGGGGGAAATCC 706
Db |||||
QY 541 CCATCAGCTGGAGACCCAGGCCACATCCAGGAGTGAAGCACCCCGAGTGTCTTCCAGC 600
Db |||||
QY 707 CCATCCGCTGGAGACCAAGACCCACATCCAGGAGTGCAACACCCCGAGTGTCTCCAGC 766
Db |||||
QY 601 ACGGAGACAAGCTTCGGCTCTCTGTTGACGTGGTGTATCTCATCTCCCTGCT 660
Db |||||
QY 767 ATGGAGACAAGCTTCGGCTCTCTGTTGATGTGGTGTATCTCATCTCCCTGCT 826
Db |||||
QY 661 CTTCTCTCTCTGCGCCCGCTCACTCTCTCGAGGCTTCTGCTGAGAACGAGTTTGG 720
Db |||||
QY 827 CTTCTCTCTGCTGCGCCCGCTCACTGCTCCGTTGGCTTCTGCTGAGAACGAGTTTGG 886
Db |||||
QY 721 GGTTCATGTGGCGGAGCGGAGCGGTCATCAGCTGTGGAGCGGCTGGAATTTGTCA 780
Db |||||
QY 887 TATTCATGTGGCGGCGGCGGTCGGGAAATCAGCTCTGGGAGCGCTGGAGTTGTCA 946
Db |||||
QY 781 ATGCTGTGATCATCTGCTGTACACGAGTGTCTCACCATCTCGGCGACCATCATCA 840
Db |||||
QY 947 ATGCTGTGATCATCTGCTGTACACGAGTGTCTCACCATCTCGGCGACTGTGATGA 1006
Db |||||
QY 841 AGATCGGATCGAGCCAAAGACTTGGGAGCTAGCAGTGTGAGCATCTCTCGGCGCA 900
Db |||||
QY 1007 AGATTGGATTTAGGCAAAAGACTTAGCCAGTATGATGTCTGCAAGTATCTCTTGGGTA 1066
Db |||||
QY 901 CCTCGACCTCTGTGTGGGTGGCGGTGATCCGCTACTGACCTTCTTCCACAACTACA 960
Db |||||
QY 1067 CCTCCACTCTGATGTGGGTGGGTGATCTGCTACTCTGACATTTTCCAAAGTACA 1126
Db |||||
QY 961 ATATCCTCATCCACACTCGGCTGGCGCTGCGGAGCTCATGGCTTCTGCTGCTGCG 1020
Db |||||
QY 1127 ACATCTTGAATGCCACGTTGGAGTGGCACTGCCAGTGTGATGCTGCTGCTGCTG 1186
Db |||||
QY 1021 TGGCTGTCACTACTCGGCTACTGCTTCTGCTGGCTGATGCTGCGGCGCTTATCATG 1080
Db |||||
QY 1187 TGGCTGTCACTACTCGGCTATGCTTCTGCTGGCTGGAGTCTTAGGGCCCTACCATG 1246
Db |||||
QY 1081 TGAAGTTCCGCTCACTCTCCA 1101
Db |||||
QY 1247 TGAAGTTCCGCTCGTGTCCA 1267
Db |||||
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RESULT 10

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US-09-796-753-161
; Sequence 161, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
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; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 161
; LENGTH: 1912
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-753-161
```

```
Query Match 18.5%; Score 203.8; DB 11; Length 1912;
Best Local Similarity 63.7%; Pred. No. 5.1e-47;
Matches 310; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
```

```
QY 615 TTCCGGCTCCTGTTTGACGTGTGTCTCATCTCCAGCTGCTCCCTGCTCTCTCTCTCTGC 674
Db |||||
QY 40 TACATGATGATCTTTGATGCTTTGTCATCTGCTTGTGTTTCAATTAATCTCTGC 99
Db |||||
QY 675 GCCCGCTCACTCCTTCGAGGCTTCTGTGCGAAGAGTGTGTGGGGTTCATGTGGCGG 734
Db |||||
QY 100 ATTAGATCTGTGATTAGAGGACTTCAGCTTCAGCAGAGTGTGTCAATTTTCTCTCTC 159
Db |||||
QY 735 CACCGGGGAGGCTCATAGCCTGTGGAGCGGCTGGAATTTGTCAATGGCTGTATCATC 794
Db |||||
QY 160 CATTATAGAAGGAGTCTTCTGTTTCTGATCAAAATGGAATTTGTCAATGATGTACATT 219
Db |||||
QY 795 CTGCTCGTCCAGCGCATGTGTCCACCATCTCGGCGACCATCATGAAGATCGGCATCGAG 854
Db |||||
QY 220 ATGATTATTATTAGTGACATATTGACAAATCATTTGGATCAATTTCTAAATAATGGAATCCAA 279
Db |||||
```

```

QY 855 GCGAAGACTTGGGAGCTACGAGCTCTGAGATCTCTGGGACCTCGAGCTGCTG 914
Db 280 GCTAAGAGTCTAAGTATGATGCTGAGCATACTTCTGGGACTTCTACCATGCTT 339
QY 915 GTGTGGTGGGCTGATCCGCTACCTGACCTTCTTCCACAACCTACAAATATCCTCATCGCC 974
Db 340 GTGTGGCTGGAGTATCCGATACCTCGGTTCTTTGCAAGTACAACTCTCTCATTTTG 399
QY 975 ACATCGGGTGGCCCTGCCAGCGTCATCGGCTTCTGTGCTGCGTGGCTGTCACTAC 1034
Db 400 ACCCTTCAGCAGCGCTGCCAATGTTCATCAGGTTCTGTGCTGTGCGAGCTAGATTTAC 459
QY 1035 CTGGGCTACTGCTCTGTGCTGATCGTCTGGGGCCCTATCATGTGAAGTTCCGCTCA 1094
Db 460 TTAGGTTACTGCTTCTGTGATGATCGTCTGGGGCCCTTACCATGACAAAGTTTCGTTCT 519
QY 1095 CTCTCCA 1101
Db 520 CTGAACA 526

```

RESULT 11

US-10-114-153-23

Sequence 23, Application US/10114153

Publication No. US20030185815A1

GENERAL INFORMATION:

APPLICANT: Padigar, Muralidhara

APPLICANT: Shenoy, Suresh

APPLICANT: Kekuda, Ramesh

APPLICANT: Rastelli, Luca

APPLICANT: Mezes, Peter

APPLICANT: Smithson, Glenda

APPLICANT: Guo, Xiaojia

APPLICANT: Gerlach, Valerie

APPLICANT: Casman, Stacie

APPLICANT: Boldog, Ferenc

APPLICANT: Li, Li

APPLICANT: Zarhusen, Bryan

APPLICANT: Tchernev, Velizar

APPLICANT: Gangoli, Esha

APPLICANT: Vernet, Corine

APPLICANT: Spytek, Kimberly

APPLICANT: Malyankar, Uriel

APPLICANT: Patturajan, Weera

APPLICANT: Miller, Charles

APPLICANT: Taupier, Raymond J. Jr.

APPLICANT: Heyes, Melvyn

APPLICANT: Ju, Jingfang

APPLICANT: Peyman, John

APPLICANT: Catterton, Elina

APPLICANT: MacDougall, John

APPLICANT: Edinger, Shlomit

APPLICANT: Stone, David

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

APPLICANT: Mazur, Ann

```

; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 23
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1663)
US-10-114-153-23

```

Query Match 18.1%; Score 199.8; DB 12; Length 1671;

Best Local Similarity 56.2%; Pred. No. 6.5e-46;

Matches 398; Conservative 0; Mismatches 304; Indels 6; Gaps 1;

```

QY 386 CTTGACGCTCAAAATCCACAAGCTGTGTCATGTCACCATCCACTTCCGGCTGAAGACCAT 445
Db 576 CTTGACGCTGGAATTTTATCGGCTCTTACAGGTGAAATCTCTTTTCATCTTAAAGCAT 635
QY 446 TAACTCCAGAGCTCATCAATAATGAGATCCGGACTGCTATACCTTCAGCGTCTCTGAT 505
Db 636 TGACCTACAGACAATTCATTCCCGTGAGTTACAGACTGTTATGCTTTTCAGAATACGAT 695
QY 506 CAGCTTTGACAAAGACACAGTGGGGGGATCCCATCAGGCTGAGACCCAGGCCCA 565
Db 696 TATCTTTGACAAATGAGCTCAGTGGGCAAAATCAAAATCTATTTTACAGTATGCCAA 755
QY 566 CATCAGGAGTGTAAAGACCCCGAGTGTCTCCAGCAGGAGACAACAGCTTCCGG---- 620
Db 756 AATTGAGATGTAAAGATTTGACATATTTGATGATGCTCAGAAAATGCTCAGTATGT 815
QY 621 -CTCCTGTTGAGCTGGTGTCTCCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 679
Db 816 CTTGCTGTTGATGATTTGTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 875
QY 680 CTCACCTCTTCAGGCTTCTGCTGACAGAACAGTTGTTGGGGTTCATGTTGGGGCAGCG 739
Db 876 ATCCATTGTTCTGCTCTAAGGTTACGGAAGAGATTTCTAAATTTCTCTCGGAGAAGTA 935
QY 740 GGGACGGGTTCATCAGCCTGTGGGAGCGGCTGGAATTTGTCATGCTGCTGCTGCTGCTGCT 799
Db 936 CAGCGGCTGTGTGACACCGACCGAGTGGAGTTTCATCAACGGCTGTTATGCTGCTGCTGCT 995
QY 800 CTTACACGAGTGTCTCACCATCTCGGGACCATCATGAAGATCGGATCGAGGCCAA 859
Db 996 GATTATCAGCGACCTTAATGACAATCATTTGGCTCCATATTAAATAATGAAATCAAAACAAA 1055
QY 860 GAACCTGGGAGTACGAGCTGTGAGCATCTCTCTGGGACCTCGACGCTGCTGCTGCTGCTG 919
Db 1056 GAATCTCAAAACTATGATCTCTGAGCAATTTTCTTGAACCTCTACGCTCTGCTGCTGCTG 1115
QY 920 GGTGGGCTGATCCGCTACCTGACCTTCTTCCACAACATACAATATCTCATCGCCACACT 979
Db 1116 GGTGAGTATCAGATACCTCGGTTATTTCCAGCATATAATGATGATTTTAAACAT 1175
QY 980 GCGGTGGCCCTGCCAGGCTCATCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039
Db 1176 GCAGGCTCAGTCCCAAAAGTTCTTCGGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1235
QY 1040 CTACTGCTTCTGCTGCTGATCGTCTGGGGCCCTCATCATGTTGAAGTT 1087
Db 1236 TTACACATTTCTGCTGCTGATTTGCTTAGGACCATACCATGACAAGTT 1283

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RESULT 12

US-10-114-153-27

```

; Sequence 27, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Hayes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACIDS AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; PRIORITY FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 27
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(1791)
US-10-114-153-27

Query Match          18.1%; Score 199.8; DB 12; Length 2067;
Best Local Similarity 56.2%; Pred.No. 6.9e-46;
Matches 398; Conservative Indels   6; Gaps    1;
OY      386 CCTCACGCTCAATTCACAAAGTGGTGCAATGTCCACCATTCTCGGCTGAAGACCAT 445

```

```
/ APPLICANT: Ju, Jingfang
/ APPLICANT: Peyman, John
/ APPLICANT: Catterton, Blina
/ APPLICANT: MacDougall, John
/ APPLICANT: Edinger, Shlomit
/ APPLICANT: Stone, David
/ APPLICANT: Mazur, Ann
/ TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACID
/ TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
/ FILE REFERENCE: 21402-322A
/ CURRENT APPLICATION NUMBER: US/10/114,153
/ CURRENT FILING DATE: 2002-08-06
/ PRIOR APPLICATION NUMBER: 60/281086
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282020
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: 60/282930
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283512
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/283444
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/283657
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283710
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283678
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284234
/ PRIOR FILING DATE: 2001-04-17
/ Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 251
/ SEQ ID NO 25
/ LENGTH: 2130
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (31)..(1645)
/ US-10-114-153-25

Query Match      18.1%   Score 199.8;   DB 12;   Length 2130;
Best Local Similarity 56.2%;   Pred. No. 7e-46;
Matches 398;   Conservative 0;   Mismatches 304;   Indels 6;   Gaps 1;

QY 386  CCTCAGCTCAAAATTCACAGCTGGTCAATGCACCATCCACTTCGGGTGAAGACCAT 445
DB 576  CTTGAGCTGGAATTTATCGGCTCTACAGGTGAATCTCTTTCATCTTAAGGCAT 635
QY 446  TAACCTCCAGAGCTCATCAATATGATCCCGAGTCCCGACTGTATACCTTCAGCGTCTGAT 505
DB 636  TGACCTACAGACAATTCATTCGCGTGAAGTACCAGACTGTATGCTTTTCAGAATACGAT 695
QY 506  CAGGTTTGACAAACAGACACAGTGGCGGATCCCATCAGCTGAGACCCAGGCCCA 565
DB 696  TATCTTTGACAAATAAGCTCACAGTGCCAAATCAAAATCTATTTTGACAGTATGCCAA 755
QY 566  CATCCAGGAGTGAAGCAACCCAGTGTCTTCCAGCAGGAGACAAAGCTTCGCGG----- 620
DB 756  AATTGAAGATGTAAGACTTGAACATTTTGATGATGATGATGATGATGATGATGATGATGAT 815
QY 621  -CTCCTGTTTACGCTGGTGTGATCTCCTCAGCTGCTCCCTGCTCTCTCTCTCTCTCTCTCT 679
DB 816  CCTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 875
QY 680  CTCACCTCTTCGAGGCTTCTGCTGAGACAGAGTTTGTGGGTTCATGTGGCGGAGCG 739
DB 876  ATCCATGTTCTTCTGCTCTAAGGTTACGGAAGAGATTTCTAAATTTCTCTCTGAGAAGTA 935
QY 740  GGGACGGGTATCAGCGCTGTGGGAGCGCTGGGAATTTGTCAGTGGTGGTACATCTGCT 799
```

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DB 936  CAAGCGGCTGTGTGTGACACCGACCGAGTGGGAGTTTCATCAACGGCTGGTATGTCCTGGT 995
QY 800  CGTCACACGAGATGTGCTCACCATCTCGGCAACCATCATCAAGATCGGATCGAGGCCAA 859
DB 996  GATTATCAGCGACCTAATGACAATCATTTGGCTCCATATTAAAAATGAAATCAAGCAAA 1055
QY 860  GAATTTGGGAGCTAGCAGCTCTGACGATCTCTCTGGGACCTCTCTGGGACCTCGACGCTGCTGTG 919
DB 1056  GAATCTCAAACTATGATCTCTGACGATTTTCTTGGAACTCTACGCTCTTGGTTTG 1115
QY 920  GGTGGGCGTATCCGCTACCTGACCTTCTTCCACAACTACAATATCTCATCGCCACT 979
DB 1116  GGTGGAGTCATCAGATACCTGGTTATTTCAGGATATATGTAATGTAATTTAAACAT 1175
QY 980  GCGGTGGGCGCTGCCAGCGTCAATGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039
DB 1176  GCAGGCGCTCACTGCCAAAGTTCTTCGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1235
QY 1040  CTAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1087
DB 1236  TTACACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1283
```

RESULT 14

```
US-10-305-810-4
/ Sequence 4, Application US/10305810
/ Publication No. US20030176385A1
/ GENERAL INFORMATION:
/ APPLICANT: Ju, Jingfang
/ APPLICANT: Huang, Chunli
/ APPLICANT: Zhong, Haihong
/ APPLICANT: Simons, Jan Fredrik
/ APPLICANT: Tailon, Bruce E.
/ APPLICANT: Chant, John S.
/ APPLICANT: Peyman, John A.
/ APPLICANT: Smithson, Glennada
/ APPLICANT: Millet, Isabelle
/ TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN EXPRESSION
/ FILE REFERENCE: 21402-501
/ CURRENT APPLICATION NUMBER: US/10/305,810
/ CURRENT FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/334,148
/ PRIOR FILING DATE: 2001-11-29
/ PRIOR APPLICATION NUMBER: 60/336,572
/ PRIOR FILING DATE: 2001-12-04
/ PRIOR APPLICATION NUMBER: 09/625,634
/ PRIOR FILING DATE: 2000-07-26
/ PRIOR APPLICATION NUMBER: 60/192,838
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: 60/194,256
/ PRIOR FILING DATE: 2000-04-03
/ PRIOR APPLICATION NUMBER: 09/957,187
/ PRIOR FILING DATE: 2001-09-19
/ PRIOR APPLICATION NUMBER: 60/233,798
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 09/970,813
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: 60/182,637
/ PRIOR FILING DATE: 2000-02-15
/ PRIOR APPLICATION NUMBER: 60/240,316
/ PRIOR FILING DATE: 2000-10-13
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 4
/ LENGTH: 1677
/ TYPE: DNA
/ ORGANISM: Ion Transport Channel (Ag 1987)
/ US-10-305-810-4
```

```
Query Match      16.7%   Score 183.8;   DB 12;   Length 1677;
Best Local Similarity 56.3%;   Pred. No. 2e-41;
Matches 388;   Conservative 0;   Mismatches 292;   Indels 9;   Gaps 2;
```

```
QY 399 TTCCACAGCTGCTCAATGTCACCATCCACTCCGGCTGAAGACCAATTAACCTCCAGGC 458
Db 586 TTATTCAGGCTCTTACAGGTTGAAATCTCCTTTTCATCTTAAAGGCAATGACCTACAGACA 645
QY 459 CTCATCAATATGAGATCCCGGACTGCTGTATACCTTCAGCGTCTGTGATCAAGTTTGACAAC 518
Db 646 ATTCATTCGGTGAGTTACCGAGCTGTATGCTTTTCAGATACGATATCTTTTGACAAT 705
QY 519 AAGCACACAGTGGCGGATCCCATCAGCTCGAGACCCAGGCCCCACATCCAGAGTGT 578
Db 706 AAGCTCACAGTGGCGGCAAAATCAAAATCTATTTCAGATGATGCCAAAATGGAAGATGT 765
QY 579 AAGCACCCAGTCTTCCAGCAGGAGACACAGCTTCCGGCTCCCTGTTGAGTGGTG 638
Db 766 AAGACTTGACATATT-----TGGATCTAGTAGTATGCTCTGGTGTGTTGATGCAATTT 819
QY 639 GTCATCTCCACCTGCTCCTCTCTCTGCGGCCGCTCACTCCCTCGAGGCTTC 698
Db 820 GTCATCTGATTTGCTGGCATCTCTATTCTGTGTACAGATCCATTGTTCTGCTCTA 879
QY 699 CTGCTGCAGAACGATTTGTTGGGCTTCATGTGGCGGAGCGGACCGGTCAATCAGCCTG 758
Db 880 AGGTTACGGA---GATTTCTAAATTTCTCTCTGGAAGTACAAGCGGCTGTGTGTGAC 936
QY 759 TGGAGCGGCTGGAATTTGTCATGGCTGGTGTACATCTCTGTGTCACAGGAGTGTCTC 818
Db 937 ACCGACAGTGGAGTTTCATCAACGGCTGGTGTCTCTGTGATTAACGAGCACTAATG 996
QY 819 ACCATCTCGGGCACCATCATGAAGATCGGCATCGAGGCCAAGAACTTTGGCGAGCTACGAC 878
Db 997 ACAATCATGGCTCCATATTAAATATGAAATCAAGCAAAAGATCTCAAAACTATGAT 1056
QY 879 GTCTGAGCATCTCTCGGGACCTCGACGCTGTGTGTGGTGGCGGTGATCCGGTAC 938
Db 1057 CTCTGCAGCAATTTCTTGAACCTCTACGCTCTTGTGTTGGTGGTGGTGTGAGTCAATCAGATAC 1116
QY 939 CTGACCTTCTTCCACAACTCAATATCTCATCGCCACATCGGGTGGCCCTGCCAGC 998
Db 1117 CTGGTTATTTCAGGCATATATGATCTGATTTTAAACAATCGAGGCTCACTGCCAAA 1176
QY 999 GTCATGGCTTCTGCTGCTGGTGTGTATCTACCTGGCTACTGCTTCTGTGGCTGG 1058
Db 1177 GTCTTCGGTTTGTGCTGTGGTGTATGATTTATCTGGTTACACATCTGTGGCTGG 1236
QY 1059 ATCGTCTGGGCGCTATCATGTGAAGTT 1087
Db 1237 ATTGTCTTAGGACCATACCATCTACAGTT 1265
```

RESULT 15

```
US-10-114-153-21
; Sequence 21, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangelli, Esba
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
```

```
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: Macdougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC AC
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 21
; LENGTH: 1677
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(1645)
; US-10-114-153-21
```

Query Match 16.7%; Score 183.8; DB 12; Length 1677;

Best Local Similarity 56.3%; Pred. No. 2e-41;

Matches 388; Conservative 0; Mismatches 292; Indels 9; Gaps 2;

```
QY 399 TTCCACAGCTGCTCAATGTCACCATCCACTCCGGCTGAAGACCAATTAACCTCCAGGC 458
Db 586 TTATTCAGGCTCTTACAGGTTGAAATCTCCTTTTCATCTTAAAGGCAATGACCTACAGACA 645
QY 459 CTCATCAATATGAGATCCCGGACTGCTGTATACCTTCAGCGTCTGTGATCAAGTTTGACAAC 518
Db 646 ATTCATTCGGTGAGTTACCGAGCTGTATGCTTTTCAGATACGATATCTTTTGACAAT 705
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QY 579 AAGCACCCAGTGTCTTCCAGCAGGAGACAAAGCTTCCGGCTCCTGTTGAGTGGTG 638
Db 766 AAGACTTGACATATT-----TGGATCTAGTAGTATGCTCTGGTGTGTTGATGCAATTT 819
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QY 699 CTGCTGCAGAACGATTTGTTGGGTTTCATGTGGCGGAGCGGAGCGGTCAATCAGCCTG 758
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Qy	819	ACCATCTCGGGCACCCATCATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGAC	878
Db	997	ACANTCATTTGGCTCCATATTAAATGGAATCAAGCAAGAAATCTCAAAACTATGAT	1056
Qy	879	GTCTGACGATCCCTCTGGGCACCTCGACGCTGCTGGTGGTGGGCGTGATCCGCTAC	938
Db	1057	CTCTGACGCAATTTTCTTGAACCTCTACGCTCTTGGTTTGGTTGGAGTCATCAGATAC	1116
Qy	939	CTGACCTTCTTCACAACTACATATCCTCATCGCCACACTGCGGGTGGCCCTGCCGAGC	998
Db	1117	CTGGGTTATTTCCAGGCATATAATGTACTGATTTTAAATGCAAGGCGCTCACTGCCAAA	1176
Qy	999	GTCAATGGCTTCTGCTGCTGGGCTGTGATCTACCTGGGCTACTGCTTCTGTGGCTGG	1058
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Qy	1059	ATCGTGTGGGCGCCCTATCATGTGAAGTT	1087
Db	1237	ATTGTCTTAGGACCATACCATCTACAGTT	1265

Search completed: October 27, 2003, 18:02:30
Job time : 364.801 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:28:31 ; Search time 357.835 Seconds
(without alignments)
8305.735 Million cell updates/sec

Title: US-09-851-494B-2_COPY_400_1500

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1101	100.0	1740	24	Human TLCC-2 prote
2	1101	100.0	1740	24	Human TRP-like cal
3	1101	100.0	2095	24	Human TLCC-2 prote
4	1101	100.0	2095	24	Human TRP-like cal
5	1100.6	100.0	2092	24	Human polynucleoti
6	1100.2	99.9	2094	21	Human secreted pro
7	1099.4	99.9	2052	22	Human membrane ass
8	1099	99.8	1741	22	Human polynucleoti

C	9	1032.4	93.8	1619	22	AAI61022	Human polynucleoti
	10	851.4	77.3	1827	24	ABL35079	Murine cDNA isolat
	11	642.2	58.3	2092	23	AA572274	DNA encoding novel
	12	539.6	49.0	734	24	ABL89699	Human polynucleoti
	13	458	41.6	499	23	AA572273	DNA encoding novel
	14	334	30.3	635	23	AA589318	DNA encoding novel
	15	282.8	25.7	776	23	AA565931	DNA encoding novel
	16	279.8	25.4	361	22	AAK62222	Human immune/haema
	17	260.8	23.7	1762	22	AAH14814	Human cDNA sequenc
	18	244.8	22.2	2860	23	AA565933	Human immune/haema
	19	203.8	18.5	1912	22	AA501697	Human TANGO 430 CD
	20	199.8	18.1	1671	25	ABX56272	Human NOV95 CG9070
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	22	199.8	18.1	2130	25	ABX56273	Human NOV9c CG9070
	23	183.8	16.7	1677	25	ABX56271	Human NOV9a CG9070
	24	169	15.3	11365	22	AAK73827	Human immune/haema
	25	159.6	14.5	20046	22	AAK73826	Human immune/haema
	26	121.2	11.0	2194	23	ABL29717	Human secreted pro
	27	107.8	9.8	492	22	ABA08523	Drosophila melanog
	28	104.8	9.5	318	23	AA589310	DNA encoding novel
	29	84.8	7.7	5035	23	ABL29716	Drosophila melanog
	30	78	7.1	415	22	AAK58837	Human immune/haema
	31	70	6.4	830	22	AAH07480	Human cDNA clone (
	32	62	5.6	1296	24	ABQ67797	Listeria innocua D
	33	62	5.6	1311	24	ABQ67800	Listeria innocua D
	34	62	5.6	319630	24	ABQ67194	Listeria innocua c
	35	62	5.6	3011208	24	ABQ69245	Listeria innocua D
	36	58.4	5.3	319	22	AAD20248	Rat integrin modul
	37	57.4	5.2	2944528	24	ABA03041	Listeria monocytog
	38	56	5.1	12411	24	ABK91613	Modified HIV prote
	39	55.8	5.1	13095	25	ABX07542	S. pneumoniae type
	40	55.8	5.1	13152	25	ABX07541	S. pneumoniae type
	41	55.8	5.1	14328	25	ABX07543	S. pneumoniae type
	42	55.8	5.1	2162598	25	ABX56454	Streptococcus pneu
	43	55.6	5.0	2940	21	AAA36699	Humanised F-RSV/HN
	44	55.6	5.0	3106	21	AA33696	Humanised F-RSV/HN
	45	54	4.9	2634	19	AAV23480	Pseudomonas Oriv s

ALIGNMENTS

RESULT 1
ABL40755
ID ABL40755 standard; cDNA; 1740 BP.

XX ABL40755;

AC AC

XX DT

03-JUL-2002 (first entry)

XX DE

Human TLCC-2 protein coding sequence.

XX KW

Transient receptor potential like calcium channel; TRP; TLCC-2; human;

XX KW

neuroprotective; analgesic; norepinephrine; antiparkinsonian; antidepressant;

XX KW

cerebroprotective; anxiolytic; antitumor; anticonvulsant; gene therapy;

XX KW

calcium signaling; Gene; ss.

XX OS

Homo sapiens.

XX FH

Key

Location/Qualifiers

FT CDS

1..1740

/tag= a

/product= "TLCC-2"

/note= "transient receptor potential-like calcium channel"

XX US200203056-A1.

XX PD

21-MAR-2002.

XX PF

06-APR-2001; 2001US-0828466.

XX PR

07-APR-2000; 2000US-0544797.

XX (CURT/) CURTIS R A J.
 PA (SILO/) SILOS-SANTIAGO I.
 XX
 PI Curtis RAJ, Silos-Santiago I;
 XX
 DR WPI; 2002-339931/37.
 DR P-PSDB; ABB07816.
 XX
 XX New nucleic acid designated TLCC-2 encodes a transient receptor
 PT potential-like calcium channel and is useful to diagnose and treat pain
 PT disorders and central nervous system neurodegenerative and neurological
 PT disorders
 XX
 XX Claim 1; Fig 1A-B; 70pp; English.
 PS
 XX The invention relates to a novel transient receptor potential (TRP)-like
 CC calcium channel, designated TLCC-2 and polynucleotides encoding the
 CC TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The
 CC TLCC-2 polypeptide, polynucleotides and modulators are useful for
 CC treating central nervous system disorders such as neurodegenerative
 CC disorders for example Alzheimer's disease, Parkinson's disease, multiple
 CC sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy,
 CC epilepsy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial
 CC infantile convulsions, paroxysmal choreoathetosis, psychiatric disorders
 CC such as depression, anxiety, schizophrenia, psychoses, mania or phobic
 CC disorders, learning or memory disorders such as amnesia, age-related
 CC memory loss, or a neurological disorder such as migraine. The molecules
 CC are also useful to treat a pain disorder. The present sequence represents
 CC the coding sequence of the human TLCC-2 polypeptide.
 XX
 XX Sequence 1740 BP; 319 A; 578 C; 475 G; 368 T; 0 other;
 SQ

Query Match 100.0%; Score 1101; DB 24; Length 1740;
 Best Local Similarity 100.0%; Pred. No. 1.8e-239;
 Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCCGGAGAGAACACCATCCCTCCGACACCTCTTCTCTGGGCTACTCGGACG 60
 DB 275 CATTCCCGGAGAGAACACCATCCCTCCGACACCTCTTCTCTGGGCTACTCGGACG 334

QY 61 GAGCGGATGACACCTTCGCGACCTACACGCGGGAGCAGCTGTACGAGCCATCTTCCATG 120
 DB 335 GAGCGGATGACACCTTCGCGACCTACACGCGGGAGCAGCTGTACGAGCCATCTTCCATG 394

QY 121 CTGTGGACCACTACTCGCGTGTGCTGACGCTGCTGACGCTGCTGACGCTGCTGACGCTG 180
 DB 395 CTGTGGACCACTACTCGCGTGTGCTGACGCTGCTGACGCTGCTGACGCTGCTGACGCTG 454

QY 181 GTGGGGGTGACCTTGGACCAATGGCTCAGGCTTGTCTCTGCGAGGCTACTACCAACC 240
 DB 455 GTGGGGGTGACCTTGGACCAATGGCTCAGGCTTGTCTCTGCGAGGCTACTACCAACC 514

QY 241 GAGCCACGTGGACCGGCCAACACACATTTGACATTTGACATTTGACATTTGACATTTGACAT 300
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QY 301 GCATCCAGTGGATCCCGGAGCGGCCCTCCGCGCCCGCCGAGCGAGATCTCAACCTCT 360
 DB 575 GCATCCAGTGGATCCCGGAGCGGCCCTCCGCGCCCGCCGAGCGAGATCTCAACCTCT 634

QY 361 TGGAAAGCAGCTCCAGTTACAGAACCTCAGCTCAATTCACAAAGCTGGTCAATGCA 420
 DB 635 TGGAAAGCAGCTCCAGTTACAGAACCTCAGCTCAATTCACAAAGCTGGTCAATGCA 694

QY 421 CCATCCACTTCCGGCTGAAGACCAATTAACTCCAGAGCTCATCAATAAGATCCCGG 480
 DB 695 CCATCCACTTCCGGCTGAAGACCAATTAACTCCAGAGCTCATCAATAAGATCCCGG 754

QY 481 ACTGCTATACCTTCAGCGTCTGTATACGTTTGTGACAAAGACACACAGTGGCGGATCC 540
 DB 755 ACTGCTATACCTTCAGCGTCTGTATACGTTTGTGACAAAGACACACAGTGGCGGATCC 814

QY 541 CCAATCAGCTTGGAGACCCAGGCCCAACATCCAGGAGTGTAAAGCACCCAGTGTCTTCCAGC 600
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QY 601 ACGGAGACACAGCTTCCGGCTCCTGTTTACGTTGGTGTATCCTCACCTGCTCCCTGT 660
 DB 875 ACGGAGACACAGCTTCCGGCTCCTGTTTACGTTGGTGTATCCTCACCTGCTCCCTGT 934

QY 661 CTTTCTCTCTCTCGCCCGCTCACTCTCTCGAGCTTCTGCTGCGAAGAGAGTTTCTGG 720
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QY 721 GGTTCATGTGGCGACGCGGACCGGTATCAGCTGTGCGAGCGCTCGAAATTTCTCA 780
 DB 995 GGTTCATGTGGCGACGCGGACCGGTATCAGCTGTGCGAGCGCTCGAAATTTCTCA 1054

QY 781 ATGGCTGTATCATCTCTGCTCACCAGCATGTGCTCAGCATCTCGGACCATCATGA 840
 DB 1055 ATGGCTGTATCATCTCTGCTCACCAGCATGTGCTCAGCATCTCGGACCATCATGA 1114

QY 841 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGCTCTGCGACATCTCTCTGGCA 900
 DB 1115 AGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACGCTCTGCGACATCTCTCTGGCA 1174

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 DB 1235 ATATCTCTCATCGCCACACATCCGCGGTGGCCCTGCCAGCGTATCGGCTTCTGCTGCTGG 1294

QY 1021 TGCTGTATCTACCTGGGCTACTGCTTCTGCTGCTGATGCTGCTGGGCGCCCTATCATG 1080
 DB 1295 TGCTGTATCTACCTGGGCTACTGCTTCTGCTGCTGATGCTGCTGGGCGCCCTATCATG 1354

QY 1081 TGAAGTTCCGCTCAGCTCTCCA 1101
 DB 1355 TGAAGTTCCGCTCAGCTCTCCA 1375

RESULT 2
 AAI71700
 ID AAI71700 standard; cDNA; 1740 BP.
 XX
 AC AAI71700;
 XX
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human TRP-like calcium channel TLCC-2 coding sequence #2.
 XX
 KW Human; TLCC-2; TRP-like calcium channel; membrane excitability;
 KW nociception; nontopic; neuroprotective; antiparkinsonian; cyostatic;
 KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;
 KW Parkinson's disease; Huntington's disease; multiple sclerosis;
 KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
 KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.
 XX
 OS Homo sapiens.
 PH
 FT Key Location/Qualifiers
 CDS 1..1740
 FT /*tag= a
 FT /product= "TLCC-2"
 FT /partial
 XX
 DN WO200177331-A1.
 XX
 XX 18-OCT-2001.
 PD
 PF 06-APR-2001; 2001WO-US11442.
 XX
 XX 07-APR-2000; 2000US-0544797.
 PR

XX (MILL-) MILLENIUM PHARM INC.
 PA Curtis RAJ, Silos-Santiago I;
 XX WPI; 2002-010913/01.
 XX P-PSDB; AAM51858.
 XX Novel isolated human transient receptor potential-like calcium channel
 PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,
 PT pain disorder, and cancer -
 XX Claim 1; Fig 1; 148pp; English.
 XX The present invention relates to the protein and coding sequences of
 CC human transient receptor potential (TRP)-like calcium channel protein-2
 CC (TLCC-2). The sequences can be used in the treatment of TLCC-2 related
 CC disorders, including central nervous system disorders such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis,
 CC Gilles de la Tourette's syndrome, autonomic function disorders, learning
 CC or memory disorders, pain disorders and disorders of cellular
 CC proliferation, including cancer. The present sequence is the TLCC-2
 CC coding sequence.
 XX Sequence 1740 BP; 319 A; 578 C; 475 G; 368 T; 0 other;
 SQ

Query Match 100.0%; Score 1101; DB 24; Length 1740;
 Best Local Similarity 100.0%; Pred. No. 1.8e-239;
 Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCGGGAGAGAACACCATCGCCTTCGACACCTCTTCCTGGCTGGGTACTCGGAGC 60
 DB 275 CATTCCGGGAGAGAACACCATCGCCTTCGACACCTCTTCCTGGGTACTCGGAGC 334

QY 61 GAGCGGATGACCTTCGAGCTTACAGCGGGAGAGCTGTACAGGCGCATCTTCGATG 120
 DB 335 GAGCGGATGACCTTCGAGCTTACAGCGGGAGAGCTGTACAGGCGCATCTTCGATG 394

QY 121 CTGTGGACAGTACCTGGCTTGCCTGAGCTGTCACGTGGCGGCTATGCTGCTGCTG 180
 DB 395 CTGTGGACAGTACCTGGCTTGCCTGAGCTGTCACGTGGCGGCTATGCTGCTGCTG 454

QY 181 GTGGGGGTGACCTTGACCAATGGCTCAGGCTTGTCTCTGCGAGGCTACTACCAACC 240
 DB 455 GTGGGGGTGACCTTGACCAATGGCTCAGGCTTGTCTCTGCGAGGCTACTACCAACC 514

QY 241 GAGGCCACGTGGACCGCGCAAGACACATTTGACATTTGATCGAGTGGTGGTACTGACT 300
 DB 515 GAGGCCACGTGGACCGCGCAAGACACATTTGACATTTGATCGAGTGGTGGTACTGACT 574

QY 301 GCATCCAGTGGATCCCGCGAGGCGCCCTCGCGCCCGCGAGCGATCTCACCTCT 360
 DB 575 GCATCCAGTGGATCCCGCGAGGCGCCCTCGCGCCCGCGAGCGATCTCACCTCT 634

QY 361 TGGAAAGCAGCTCCAGTTTACAGAACTCCTCAGCTCAAAATTCACAGCTGGTCAATGTCA 420
 DB 635 TGGAAAGCAGCTCCAGTTTACAGAACTCCTCAGCTCAAAATTCACAGCTGGTCAATGTCA 694

QY 421 CCATCCACTTCCGGCTGAGAGACCATTAACCTCCAGAGCCTCATCAATATGAGATCCCGG 480
 DB 695 CCATCCACTTCCGGCTGAGAGACCATTAACCTCCAGAGCCTCATCAATATGAGATCCCGG 754

QY 481 ACTGCTATACCTTCAGCGTCTGTATCAGTTTGAACAAGACACAGTGGGCGGATCC 540
 DB 755 ACTGCTATACCTTCAGCGTCTGTATCAGTTTGAACAAGACACAGTGGGCGGATCC 814

QY 541 CCATCAGCTGGAGACCCAGCCACATCCAGAGTGTAGACCCCGAGTGTCTTCAGC 600
 DB 815 CCATCAGCTGGAGACCCAGCCACATCCAGAGTGTAGACCCCGAGTGTCTTCAGC 874

QY 601 ACGGAGACACAGCTTCCGGCTCCTGTTTGACCTGGTGGTCACTCCTCAGCTGCTCCCTGT 660
 DB 875 ACGGAGACACAGCTTCCGGCTCCTGTTTGACCTGGTGGTCACTCCTCAGCTGCTCCCTGT 934

QY 661 CCTTCTCTCTCTGCGCGCT 720
 DB 935 CCTTCTCTCTCTGCGCGCT 994

QY 721 GGTTCATGTGGGCGCAGCGGGACGGGTCTCATCAGCCTGTGGGAGCGCTGGAATTTGTC 780
 DB 995 GGTTCATGTGGGCGCAGCGGGACGGGTCTCATCAGCCTGTGGGAGCGCTGGAATTTGTC 1054

QY 781 ATGGCTGTGATACCT 840
 DB 1055 ATGGCTGTGATACCT 1114

QY 841 AGATCGGCATCGAGGCGCAGAACTTGGCGAGCTACACGCTCTCGAGCATCTCTCTGGGCA 900
 DB 1115 AGATCGGCATCGAGGCGCAGAACTTGGCGAGCTACACGCTCTCGAGCATCTCTCTGGGCA 1174

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 DB 1175 CCTCGACGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1234

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QY 1021 TGGCT 1080
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QY 1081 TGAAGTTCCGCTCACCTCTCCA 1101
 DB 1355 TGAAGTTCCGCTCACCTCTCCA 1375

RESULT 3

ABL40754
 ID ABL40754 standard; cDNA; 2095 BP.
 XX ABL40754;
 AC
 XX
 DT 03-JUL-2002 (first entry)
 XX
 DE Human TLCC-2 protein encoding cDNA.
 XX
 KW Transient receptor potential like calcium channel; TRP; TLCC-2; human;
 KW neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;
 KW cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy;
 KW calcium signaling; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 141..1883
 FT /*tag= a
 FT /product= "TLCC-2"
 FT /note= "transient receptor potential-like calcium
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 XX
 US2002035056-A1.
 XX
 XX 21-MAR-2002.
 XX
 XX 06-APR-2001; 2001US-0828466.
 XX
 XX 07-APR-2000; 2000US-0544797.
 XX
 XX (CURT/) CURTIS R A J.
 XX (SILO/) SILOS-SANTIAGO I.
 XX Curtis RAJ, Silos-Santiago I;
 WPI; 2002-338931/37.
 P-PSDB; ABB07816.

XX New nucleic acid designated TLCC-2 encodes a transient receptor
PT potential-like calcium channel and is useful to diagnose and treat pain
PT disorders and central nervous system neurodegenerative and neurological
PT disorders -
XX
XX Claim 1; Fig 1A-B; 70pp; English.
XX
CC The invention relates to a novel transient receptor potential (TRP)-like
CC calcium channel, designated TLCC-2 and polynucleotides encoding the
CC TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The
CC TLCC-2 polypeptide, polynucleotides and modulators are useful for
CC treating central nervous system disorders such as neurodegenerative
CC disorders for example Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy,
CC epilepsy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial
CC infantile convulsions, paroxysmal choreoathetosis, psychiatric disorders
CC such as depression, anxiety, schizophrenia, psychoses, mania or phobic
CC disorders, learning or memory disorders such as amnesia, age-related
CC memory loss, or a neurological disorder such as migraine. The molecules
CC are also useful to treat a pain disorder. The present sequence represents
CC a cDNA encoding the human TLCC-2 polypeptide.
XX
SQ Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;

Query Match 100.0%; Score 1101; DB 24; Length 2095;
Best Local Similarity 100.0%; Pred. No. 1.9e-239;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCGGGAAGAGAACACATCGCTTCGACACCTCTTCCTCGTGGGCTACTCGAGC 60
Db 415 CATTCCGGGAAGAGAACACATCGCTTCGACACCTCTTCCTCGTGGGCTACTCGAGC 474

QY 61 GAGCGGATGACACCTTCGACCTTACAGCGGGAGCAGCTGTACAGGCCATCTTCATG 120
Db 475 GAGCGGATGACACCTTCGACCTTACAGCGGGAGCAGCTGTACAGGCCATCTTCATG 534

QY 121 CTGTGGACCACTACTCGCGTGTGCTGACGTGTCACTGGGCGGTATGCGTATGTCGGTG 180
Db 535 CTGTGGACCACTACTCGCGTGTGCTGACGTGTCACTGGGCGGTATGCGTATGTCGGTG 594

QY 181 GTGGGGGTGACCTTTGGACCAATGGCTCAGGGTGTCTCTCTGCCAGCGGTACTACACC 240
Db 595 GTGGGGGTGACCTTTGGACCAATGGCTCAGGGTGTCTCTCTGCCAGCGGTACTACACC 654

QY 241 GAGGCCACGTGACCGGCCAACGACACATTGTGATTCGATTCGGTGTGTTACTGACT 300
Db 655 GAGGCCACGTGACCGGCCAACGACACATTGTGATTCGATTCGGTGTGTTACTGACT 714

QY 301 GCATCCAGGTGGATCCCTCCCGAGCGGCCCTCTCCGCCCCCGAGGACGATCTCACCCCTCT 360
Db 715 GCATCCAGGTGGATCCCTCCCGAGCGGCCCTCTCCGCCCCCGAGGACGATCTCACCCCTCT 774

QY 361 TGGAAAGCAGCTCCAGTTA CAAGAACCTCAGCTCAAAATTCACAAGTGTGTAATGTCA 420
Db 775 TGGAAAGCAGCTCCAGTTA CAAGAACCTCAGCTCAAAATTCACAAGTGTGTAATGTCA 834

QY 421 CCATCCACTTCGGGCTGAAGACCAATTACCTCCAGAGCTCATCAATTAATCAGATCCGG 480
Db 835 CCATCCACTTCGGGCTGAAGACCAATTACCTCCAGAGCTCATCAATTAATCAGATCCGG 894

QY 481 ACTGCTATACCTTCAGGGTCTCTGATCAGTTTGTACAACAAAGCACAGTGGGGGATGCC 540
Db 895 ACTGCTATACCTTCAGGGTCTCTGATCAGTTTGTACAACAAAGCACAGTGGGGGATGCC 954

QY 541 CCATCAGCCTGGAGACCCAGGCCCAATCCAGGAGTGTGAAGCACCCCACTGCTTCCAGC 600
Db 955 CCATCAGCCTGGAGACCCAGGCCCAATCCAGGAGTGTGAAGCACCCCACTGCTTCCAGC 1014

QY 601 ACGGAGACAAAGCTTCGGGCTCCTGTTTGTAGTGTGGTGTATCTCTACCTGCTCCCTGT 660
Db 1015 ACGGAGACAAAGCTTCGGGCTCCTGTTTGTAGTGTGGTGTATCTCTACCTGCTCCCTGT 1074

PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,
 PT pain disorder, and cancer -
 XX
 XX
 PS Claim 1; Fig 1; 148pp; English.
 XX
 CC The present invention relates to the protein and coding sequences of
 CC human transient receptor potential (TRP)-like calcium channel protein-2
 CC (TLCC-2). The sequences can be used in the treatment of TLCC-2 related
 CC disorders, including central nervous system disorders such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis,
 CC Gilles de la Tourette's syndrome, autonomic function disorders, learning
 CC or memory disorders, pain disorders and disorders of cellular
 CC proliferation, including cancer. The present sequence is the TLCC-2
 CC coding sequence including the 3' UTR.
 XX
 SQ Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;
 Query Match 100.0%; Score 1101; DB 24; Length 2095;
 Best Local Similarity 100.0%; Pred. No. 1.9e-239;
 Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATTCCGGGAGAGAACACCATCGCTTCGGACACCTCTTCCTGCTGGGTACTCGGAGC 60
 DB 415 CATTCCGGGAGAGAACACCATCGCTTCGGACACCTCTTCCTGCTGGGTACTCGGAGC 474
 QY 61 GAGCGGATGACCTTCGCGACCTACACGGGGAGCAGCTGTACCGAGCCACTTCCCATG 120
 DB 475 GAGCGGATGACCTTCGCGACCTACACGGGGAGCAGCTGTACCGAGCCACTTCCCATG 534
 QY 121 CTGTGGACAGTACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 DB 535 CTGTGGACAGTACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594
 QY 181 GTGGGGGTGACCTTGGACCAATGGCTTCAGGCGTGTCTCTGCGACGGGTACTACCAAC 240
 DB 595 GTGGGGGTGACCTTGGACCAATGGCTTCAGGCGTGTCTCTGCGACGGGTACTACCAAC 654
 QY 241 GAGGCGACGTGGACCGGCGCAAGACATTTGACATGATTCGATGGTGGTACTGACT 300
 DB 655 GAGGCGACGTGGACCGGCGCAAGACATTTGACATGATTCGATGGTGGTACTGACT 714
 QY 301 GCATCCAGGTGGATCCCGCGGCGGCGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCT 360
 DB 715 GCATCCAGGTGGATCCCGCGGCGGCGCCCTCGCGCGCGCGCGCGCGCGCGCGCT 774
 QY 361 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA 420
 DB 775 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAAATTCACAAAGCTGGTCAATGTCA 834
 QY 421 CCATCCACTTCGGCTGAAGACCAATTAACTCCAGAGCTCATCAATAAGAGATCCCGG 480
 DB 835 CCATCCACTTCGGCTGAAGACCAATTAACTCCAGAGCTCATCAATAAGAGATCCCGG 894
 QY 481 ACTGCTATACCTTCAGGCTCTGATCAGTTTGACACAAAGCACACAGTGGCGGATCC 540
 DB 895 ACTGCTATACCTTCAGGCTCTGATCAGTTTGACACAAAGCACACAGTGGCGGATCC 954
 QY 541 CCATCAGCTTGGAGACCCAGCGCCACATCCAGGAGTGTAAAGCACCCCGAGTGTCTTCCAGC 600
 DB 955 CCATCAGCTTGGAGACCCAGCGCCACATCCAGGAGTGTAAAGCACCCCGAGTGTCTTCCAGC 1014
 QY 601 ACGGAGACACAGCTTCGGGCTCCTGTTGACGTGGTGGTCACTCACTCAGCTGCTCCTGT 660
 DB 1015 ACGGAGACACAGCTTCGGGCTCCTGTTTGGAGTGGTGTATCTCACTGCTCCTGT 1074
 QY 661 CCTTCCTCTGCGCGGCTCACTCTCTCGAGGCTTCCTGCTGCGAAGACGAGTTTGG 720
 DB 1075 CCTTCCTCTGCGCGGCTCACTCTCTCGAGGCTTCCTGCTGCGAAGACGAGTTTGG 1134
 QY 721 GGTTTCATGTGGCGGACGGGAGCGGTTCATCAGCCTGTGGAGCGGCTGGAATTTGTCA 780
 DB 1135 GGTTTCATGTGGCGGACGGGAGCGGTTCATCAGCCTGTGGAGCGGCTGGAATTTGTCA 1194

QY 781 ATGGCTGTACATCTCTGCTCGTCCACGAGGATGTGCTCACCATCTCGGSCACCATCATGA 840
 DB 1195 ATGGCTGTACATCTCTGCTCGTCCACGAGGATGTGCTCACCATCTCGGSCACCATCATGA 1254
 QY 841 AGATCGGATCGAGGCAAGAACTTGGGAGCTACGACGCTCTCAGCATCTCTCTGGGCA 900
 DB 1255 AGATCGGATCGAGGCAAGAACTTGGGAGCTACGACGCTCTCAGCATCTCTCTGGGCA 1314
 QY 901 CCTCGACGCTGCTGTGTGGTGGGCGTGCATCGCTACCTGCTTCTTCCACAACATACA 960
 DB 1315 CCTCGACGCTGCTGTGTGGTGGGCGTGCATCGCTACCTGCTTCTTCCACAACATACA 1374
 QY 961 ATATCTCTATCGCCACACTGCGGCTGCGCTGCCAGGCTCATGCGCTTCTGCTGCTGG 1020
 DB 1375 ATATCTCTATCGCCACACTGCGGCTGCGCTGCCAGGCTCATGCGCTTCTGCTGCTGG 1434
 QY 1021 TGCTCTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGCGCTTATCATG 1080
 DB 1435 TGCTCTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGCGCTTATCATG 1494
 QY 1081 TGAAGTTCGCTCAGCTCTCCA 1101
 DB 1495 TGAAGTTCGCTCAGCTCTCCA 1515
 RESULT 5
 ABL90358
 ID ABL90358 standard; cDNA; 2092 BP.
 XX AC ABL90358;
 XX DT 24-MAY-2002 (first entry)
 XX DE Human polynucleotide SEQ ID NO 920.
 XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200190304-A2.
 XX PD 29-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-US16450.
 XX PR 19-MAY-2000; 2000US-205515P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Birse CE, Rosen CA;
 XX DR WPI; 2002-122018/16.
 XX DR P-PSDB; ABB89949.
 XX PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 XX disorders -
 PS Claim 4; SEQ ID NO 920; 2081pp + Sequence Listing; English.
 CC The invention relates to novel genes (ABL9449-ABL90853) and proteins
 CC (ABB9040-ABB9044) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;

CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence 2092 BP; 399 A; 676 C; 590 G; 425 T; 2 other;

Query Match 100.0%; Score 1100.6; DB 24; Length 2092;
 Best Local Similarity 99.9%; Pred. No. 2.4e-238;
 Matches 1100; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCGGGAAGAGAACACCATCGCTCCGACACCTCTTCTGCTGGGCTACTCGGACG 60
 DB |||||
 382 CATTCCGGGAAGAGAACACCATCGCTCCGACACCTCTTCTGCTGGGCTACTCGGACG 441
 QY 61 GAGCGGATGACACCTTCCAGCCTACACGCGGAGCAGCTGTACAGGCCATCTTCCATG 120
 DB |||||
 442 GAGCGGATGACACCTTCCAGCCTACACGCGGAGCAGCTGTACAGGCCATCTTCCATG 501
 QY 121 CTGTGGACCACTACTCTGCGCTTCTGACGTGCTACTGCGCGGTATCGGTATGTCGGTG 180
 DB |||||
 502 CTGTGGACCACTACTCTGCGCTTCTGACGTGCTACTGCGCGGTATCGGTATGTCGGTG 561
 QY 181 GTGGGGTGACCTTGGACCAATGCTCAGGCTTGCTCTCTGCCAGCGGTACTACACC 240
 DB |||||
 562 GTGGGGTGACCTTGGACCAATGCTCAGGCTTGCTCTCTGCCAGCGGTACTACACC 621
 QY 241 GAGCCACGTGGACCGCCACGACATTTGACATTTGACATTTGACATTTGACATTTGAC 300
 DB |||||
 622 GAGCCACGTGGACCGCCACGACATTTGACATTTGACATTTGACATTTGACATTTGAC 681
 QY 301 GCATCCAGTGATCCCCCGGCGGCGCCCTCCGCGCCCGGACGAGCATCTCAACCTCT 360
 DB |||||
 682 GCATCCAGTGATCCCCCGGCGGCGCCCTCCGCGCCCGGACGAGCATCTCAACCTCT 741
 QY 361 TGGAAAGCAGTCCAGTTTACAGAACCTCAGCTCAAAATTCACAAAGCTGGTCAATGTCA 420
 DB |||||
 742 TGGAAAGCAGTCCAGTTTACAGAACCTCAGCTCAAAATTCACAAAGCTGGTCAATGTCA 801
 QY 421 CCATCCACTCCGCTGAGACCATTAACCTCCAGAGCTCATCAATAGATTCGCGG 480
 DB |||||
 802 CCATCCACTCCGCTGAGACCATTAACCTCCAGAGCTCATCAATAGATTCGCGG 861
 QY 481 ACTGCTATACCTTCAGCGCTCTGATCAGTTTGACAAACAAAGCACACAGTGGCGGATCC 540
 DB |||||
 862 ACTGCTATACCTTCAGCGCTCTGATCAGTTTGACAAACAAAGCACACAGTGGCGGATCC 921
 QY 541 CCATCAGCTGGAGACCCAGGCCACATCCAGGAGTGAAGCACCCCACTCTTCCAGC 600
 DB |||||
 922 CCATCAGCTGGAGACCCAGGCCACATCCAGGAGTGAAGCACCCCACTCTTCCAGC 981
 QY 601 ACGGAGACACAGCTTCGCGCTCTGTTTGACGTTGAGTGGTCTATCTCTACCTGCTCCCTGT 660
 DB |||||
 982 ACGGAGACACAGCTTCGCGCTCTGTTTGACGTTGAGTGGTCTATCTCTACCTGCTCCCTGT 1041
 QY 661 CTTTCTCTCTGCGCGGCTCACTCTTCGAGGCTTCTCTGACAGACAGTGGTGG 720
 DB |||||
 1042 CTTTCTCTCTGCGCGGCTCACTCTTCGAGGCTTCTCTGACAGACAGTGGTGG 1101
 QY 721 GGTTCATGTGGCGGAGCGGGAAGGTCATCAGCTGTGGGAGCGGTGGAATTTGTCA 780
 DB |||||
 1102 GGTTCATGTGGCGGAGCGGGAAGGTCATCAGCTGTGGGAGCGGTGGAATTTGTCA 1161
 QY 781 ATGCTGGTATCTCTGCTGACACGAGTGTGCTCACCATCTCGGGAACCATATGA 840
 DB |||||
 1162 ATGCTGGTATCTCTGCTGACACGAGTGTGCTCACCATCTCGGGAACCATATGA 1221

QY 841 AGATCGGATCGAGGCCAAGAACTTGGGAGCTACGACGCTGCGAGCATCTCTCTGGGCA 900
 DB |||||
 1222 AGATCGGATCGAGGCCAAGAACTTGGGAGCTACGACGCTGCGAGCATCTCTCTGGGCA 1281
 QY 901 CCTCGAGCTGCTGCTGTGGTGGGCGTGATCCGCTACCTGACCTCTTCCACAACTACA 960
 DB |||||
 1282 CCTCGAGCTGCTGCTGTGGTGGGCGTGATCCGCTACCTGACCTCTTCCACAACTACA 1341
 QY 961 ATATCTCTCATGCCACACTGCGGGTGGCCCTGCCAGCGTCATCGCTTCTGTGCTGCG 1020
 DB |||||
 1342 ATATCTCTCATGCCACACTGCGGGTGGCCCTGCCAGCGTCATCGCTTCTGTGCTGCG 1401
 QY 1021 TGGTGTCTATCTACCTGGGCTACTGCTTCTGTGCTGATCGTCTGGGCGCCCTATCATG 1080
 DB |||||
 1402 TGGTGTCTATCTACCTGGGCTACTGCTTCTGTGCTGATCGTCTGGGCGCCCTATCATG 1461
 QY 1081 TGAAGTTCCGCTCACTCTCCA 1101
 DB |||||
 1462 TGAAGTTCCGCTCACTCTCCA 1482

RESULT 6
 AAA39067
 ID AAA39067 standard; cDNA; 2094 BP.
 XX
 AC AAA39067;
 XX
 DT 30-AUG-2000 (first entry)
 XX
 DE Human secreted protein gene 16 SEQ ID NO:26.
 XX
 KW Human; secreted protein; cytostatic; anti-proliferative; vulnerary;
 KW immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis;
 KW hyperproliferative disorder; infectious disease; tissue regeneration;
 KW screening; food additive; preservative; wound healing;
 KW hyper-vascular disease; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200017222-A1.
 XX
 PD 30-MAR-2000.
 XX
 PF 22-SEP-1999; 99WO-US22012.
 XX
 PR 23-SEP-1998; 98US-0101546.
 PR 02-OCT-1998; 98US-0102895.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 FI Ruben SM, Rosen CA, Duan RD, Shi Y, Lafleur DW, Young PE, Ni J;
 FI Komatsoulis G, Endress GA, Soppet DR;
 XX
 DR WPI; 2000-283538/24.
 DR P-PSDB; AAB08906.
 XX
 PT Human secreted proteins and coding sequences useful in diagnostic and
 PT therapeutic methods for disorders such as immune system or
 PT proliferative disorders, related to the proteins
 XX
 PS Claim 1; Page 331-332; 416pp; English.
 XX
 CC The polynucleotide sequences given in AAA39052 to AAA39088 encode the
 CC human secreted proteins given in AAB08891 to AAB08984. The human secreted
 CC proteins can have activities based on the tissues and cells they are
 CC expressed in. Examples of the activities are: cytostatic;
 CC anti-proliferative; immunosuppressive; antibacterial; and vulnerary. The
 CC secreted proteins and their related polynucleotide sequences are useful
 CC for diagnostic and therapeutic methods for diagnosing and treating
 CC disorders related to the secreted proteins. The proteins, and
 CC polynucleotide sequences may be useful for treating disorders of the
 CC immune system, hyperproliferative disorders, infectious disease, and
 CC regeneration of tissues, for chemotaxis and for screening molecules that

CC bind to the proteins. The proteins or polynucleotide sequences may be
CC used as food additives or preservatives, to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, co-factors or other nutritional components. Agonists or
CC antagonists of the proteins may be used to prevent scar tissue growth
CC during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051
CC and AAB08890 are sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 2094 BP; 400 A; 673 C; 589 G; 426 T; 6 other;

Query Match 99.9%; Score 1100.2; DB 21; Length 2094;
Best Local Similarity 99.8%; Pred. No. 2.9e-239;
Matches 1099; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCGGGAGAGAACACCATCGCCTTCGGACACCTCTTCCTGCTGGGTACTTCGGAGC 60
DB |||||
QY 61 GAGCGGATGACCTTCGCGAGCTTACACGGGGAGAGCTGTACCGAGCCATCTTCATG 120
DB |||||
QY 442 GAGCGGATGACCTTCGCGAGCTTACACGGGGAGAGCTGTACCGAGCCATCTTCATG 501
DB |||||
QY 121 CTGTGACCACTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB |||||
QY 502 CTGTGACCACTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561
DB |||||
QY 181 GTGGGGTGCACCTTGGACCAATGGCTCAGGGCTTGTCTCTGCGAGCGGTACTACCA 240
DB |||||
QY 562 GTGGGGTGCACCTTGGACCAATGGCTCAGGGCTTGTCTCTGCGAGCGGTACTACCA 621
DB |||||
QY 241 GAGGCCACGTGGAGCCCGGCAAGACATTTGATGATGATGATGATGATGATGATGAT 300
DB |||||
QY 622 GAGGCCACGTGGAGCCCGGCAAGACATTTGATGATGATGATGATGATGATGATGAT 681
DB |||||
QY 301 GCATCAGGTGGATCCCGGAGCGGCGCCCTCGCGCCCGGAGCGAGTCAACCTCT 360
DB |||||
QY 682 GCATCAGGTGGATCCCGGAGCGGCGCCCTCGCGCCCGGAGCGAGTCAACCTCT 741
DB |||||
QY 361 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAATTCACAAAGCTGGTCAATGCA 420
DB |||||
QY 742 TGGAAAGCAGCTCCAGTTACAAGAACCTCAGCTCAATTCACAAAGCTGGTCAATGCA 801
DB |||||
QY 421 CCATCCACTTCGGCTGAGACCACTTAACCTCCAGAGCTCATCAATGAGATCCCGG 480
DB |||||
QY 802 CCATCCACTTCGGCTGAGACCACTTAACCTCCAGAGCTCATCAATGAGATCCCGG 861
DB |||||
QY 481 ACTGCTATACCTTCAGGCTCCTGATCAGTTGACAAACAGACACAGTGGCGGATCC 540
DB |||||
QY 862 ACTGCTATACCTTCAGGCTCCTGATCAGTTGACAAACAGACACAGTGGCGGATCC 921
DB |||||
QY 541 CCATCAGCTGGAGACCCAGGCCACATCCAGAGTGTAAAGCAACCCAGTGTCTTCCAGC 600
DB |||||
QY 922 CCATCAGCTGGAGACCCAGGCCACATCCAGAGTGTAAAGCAACCCAGTGTCTTCCAGC 981
DB |||||
QY 601 ACGGAGACACAGCTTCGGCTCCTGTTGACGTGGTGTGATCCTCACTGCTCCCTGT 660
DB |||||
QY 982 ACGGAGACACAGCTTCGGCTCCTGTTGACGTGGTGTGATCCTCACTGCTCCCTGT 1041
DB |||||
QY 661 CTTTCTCTCTGCGCGCTCACTCTCTGAGGCTTCTGCTGCAAGACGAGTTTCTGG 720
DB |||||
QY 1042 CTTTCTCTCTGCGCGCTCACTCTCTGAGGCTTCTGCTGCAAGACGAGTTTCTGG 1101
DB |||||
QY 721 GGTTCATGTGGCGGAGCGGGAGCTCATCAGCTGTGGAGCGGTGGAATTTGCA 780
DB |||||
QY 1102 GGTTCATGTGGCGGAGCGGGAGCTCATCAGCTGTGGAGCGGTGGAATTTGCA 1161
DB |||||
QY 781 ATGCTGGTACATCCTGCTGCTACCGAGCTGTGCTCACCATCTCGGGACCACTATGA 840
DB |||||
QY 1162 ATGCTGGTACATCCTGCTGCTACCGAGCTGTGCTCACCATCTCGGGACCACTATGA 1221
DB |||||
QY 841 AGATCGGATCGAGCCAGAACTTGGGAGCTACGAGCTGCGAGCATCTCTCTGGCA 900
DB |||||

DB 1222 AGATCGGATCGAGGCAAGAACTTGGGAGCTACGACGTCTGCAGCATCTCTCTGGCA 1281
QY 901 CCTCGAGCGTGTGCTGGTGGGCGTGTGATCGCTACCTGCTTCTTCCACAATACA 960
DB |||||
DB 1282 CCTCGAGCGTGTGCTGGTGGGCGTGTGATCGCTACCTGCTTCTTCCACAATACA 1341
QY 961 ATATCTCATTCGCCACACTGCGGGTGGCGCTGCCAGCGTCATGCGCTTCTGCTGCG 1020
DB |||||
DB 1342 ATATCTCATTCGCCACACTGCGGGTGGCGCTGCCAGCGTCATGCGCTTCTGCTGCG 1401
QY 1021 TGCGCTCATCTACCTGGGCTACTGCTTCTGCTGGTGGATCGTGGGCGCTTATCATG 1080
DB 1402 TGCGCTCATCTACCTGGGCTACTGCTTCTGCTGGTGGATCGTGGGCGCTTATCATG 1461
QY 1081 TGAAGTTCGCTCACTCTCCA 1101
DB 1462 TGAAGTTCGCTCACTCTCCA 1482

RESULT 7
AAF81753
ID AAF81753 standard; cDNA; 2052 BP.
XX
AC AAF81753;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human membrane associated protein MEMAP-13 encoding cDNA.
KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiatherosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea; ss.
XX
OS Homo sapiens.
XX
PN WO200112662-A2.
XX
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US22315.
XX
PR 17-AUG-1999; 99US-0149641.
PR 09-NOV-1999; 99US-0164203.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
PI P-PSDB; AAB74707.
DR
DR WPI: 2001-168860/17.
DR P-PSDB; AAB74707.
XX
XX Isolated polypeptide with a human membrane associated protein sequence
PT is useful for the diagnosis, prevention and treatment of cell
PT proliferative, autoimmune/inflammatory, neurological and
PT gastrointestinal disorders -
XX
PS Claim 5; Page 157-158; 173pp; English.
XX
CC AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiatherosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders

CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated
CC with MEMAP.
XX
SQ Sequence 2052 BP; 375 A; 670 C; 582 G; 425 T; 0 other;

Sequence 2052 BP; 375 A; 670 C; 582 G; 425 T; 0 other;

Query Match 99.9%; Score 1099.4; DB 22; Length 2052;
Best Local Similarity 99.9%; Pred. No. 4.4e-239;
Matches 1100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	CATTCCGGGAAGAGAA	CACCAATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG	60
Db	382	CATTCCGGGAAGAGAA	CACCAATCGCCTTCCGACACCTCTTCTGCTGGGCTACTCGGACG	441
QY	61	GAGCGGATGACACCTT	CGACGCTACAGCGGGAGCAGCTACACGACCAATCTTCCATG	120
Db	442	GAGCGGATGACACCTT	CGACGCTACAGCGGGAGCAGCTACACGACCAATCTTCCATG	501
QY	121	CTGTGGACCAAGTACCT	CGCGTTGCGTGCATCGTGTCACTGGGCGGCTATGCGTATGTCGGTG	180
Db	502	CTGTGGACCAAGTACCT	CGCGTTGCGTGCATCGTGTCACTGGGCGGCTATGCGTATGTCGGTG	561
QY	181	GTGGGGGTGACCTTGG	ACCAATGGCTCAGGGCTTGTCTCTGCGAGGGTACTACACACC	240
Db	562	GTGGGGGTGACCTTGG	ACCAATGGCTCAGGGCTTGTCTCTGCGAGGGTACTACACACC	621
QY	241	GAGGCCACGTGGACCG	CGCGCCAAACACACATTTGACATTTGATCCGATGGTGGTTACTGACT	300
Db	622	GAGGCCACGTGGACCG	CGCGCCAAACACACATTTGACATTTGATCCGATGGTGGTTACTGACT	681
QY	301	GCATCCAGGTGGATCCC	CGGAGGGGCGCCCTTCGCGCCCGCAGGACGATCTCAACCTCT	360
Db	682	GCATCCAGGTGGATCCC	CGGAGGGGCGCCCTTCGCGCCCGCAGGACGATCTCAACCTCT	741
QY	361	TGAAAGCAGCTCCAGT	TACAAGAAACCTCAGCCTCAAATTCACAAGCTGGTCAATGTCA	420
Db	742	TGAAAGCAGCTCCAGT	TACAAGAAACCTCAGCCTCAAATTCACAAGCTGGTCAATGTCA	801
QY	421	CCATCCACTTCGGCTG	AGACCACTTAACCTTCAGAGCCTCATCAATAAGAGATCCCGG	480
Db	802	CCATCCACTTCGGCTG	AGACCACTTAACCTTCAGAGCCTCATCAATAAGAGATCCCGG	861
QY	481	ACTGCTATACCTTCAG	CGTCTGATACGTTTGACAAAGCACACAGTGGGGGATCC	540
Db	862	ACTGCTATACCTTCAG	CGTCTGATACGTTTGACAAAGCACACAGTGGGGGATCC	921
QY	541	CCATCAGCTTGGAGACC	AGGCCACATCCAGGAGTGTAAACCCAGTGTCTTTCAGC	600
Db	922	CCATCAGCTTGGAGACC	AGGCCACATCCAGGAGTGTAAACCCAGTGTCTTTCAGC	981
QY	601	ACGGAGCAACAGTTCC	GGGCTCTGTTTGACGTGGTGGTCACTCCTCACCTGTCCCTGT	660
Db	982	ACGGAGCAACAGTTCC	GGGCTCTGTTTGACGTGGTGGTCACTCCTCACCTGTCCCTGT	1041
QY	661	CTTTCCTCTCTGCGCC	CGGCTCACTCCTTCGAGGCTTCCTGCTCAGAAACGAGTTGTGG	720
Db	1042	CTTTCCTCTCTGCGCC	CGGCTCACTCCTTCGAGGCTTCCTGCTCAGAAACGAGTTGTGG	1101
QY	721	GTTTCATGTGGCGCAC	GCGGACGGTCAATCAGCCTGTGGAGCGGCTGGAATTTGTCA	780
Db	1102	GTTTCATGTGGCGCAC	GCGGACGGTCAATCAGCCTGTGGAGCGGCTGGAATTTGTCA	1161
QY	781	ATGGCTGGTACATTCCT	GCTCGTCACACAGCATGTGCTCACCATCTCGGACCAATCATGA	840
Db	1162	ATGGCTGGTACATTCCT	GCTCGTCACACAGCATGTGCTCACCATCTCGGACCAATCATGA	1221

CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX SQ Sequence 1741 BP; 320 A; 554 C; 487 G; 380 T; 0 other;

Query Match 99.8%; Score 1099; DB 22; Length 1741;
Best Local Similarity 100.0%; Pred. No. 5.2e-239;
Matches 1099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCGGGAGAGAACACCATCGCTTCGGACACTTCTCTGCTGGGCTACTCGGACGGA 62
Db 73 TTCGGGAGAGAACACCATCGCTTCGGACACTTCTCTGCTGGGCTACTCGGACGGA 132
QY 63 GCGGATGACACCTTCGACGCTACACGCGGAGCAGCTGACACGACCATCTTCCATGCT 122
Db 133 GCGGATGACACCTTCGACGCTACACGCGGAGCAGCTGACACGACCATCTTCCATGCT 192
QY 123 GTGGACAGTACCTGGCGGTTGCCGTGCTACTGGGCGGATGCGTATGCCGTGGT 182
Db 193 GTGGACAGTACCTGGCGGTTGCCGTGCTACTGGGCGGATGCGTATGCCGTGGT 252
QY 183 GGGGGTACCTTGGACCAATGCTCAGGCTTGCTCTGCCAGCGGTACTACACCGGA 242
Db 253 GGGGGTACCTTGGACCAATGCTCAGGCTTGCTCTGCCAGCGGTACTACACCGGA 312
QY 243 GGCACGTGACCGCGCCACAGCACATTGACATGATCGATGGGTTACTGCTGTC 302
Db 313 GGCACGTGACCGCGCCACAGCACATTGACATGATCGATGGGTTACTGCTGTC 372
QY 303 ATCCAGGTGATCCCCCGGACGCGCCCTCCGCGCCCGACGACGATCAACCTCTTG 362
Db 373 ATCCAGGTGATCCCCCGGACGCGCCCTCCGCGCCCGACGACGATCAACCTCTTG 432
QY 363 GAAAGCAGTCCAGTTACAGAACCTCAGCTCAAAATCCAAAGCTGGTCAATGTCACC 422
Db 433 GAAAGCAGTCCAGTTACAGAACCTCAGCTCAAAATCCAAAGCTGGTCAATGTCACC 492
QY 423 ATCCACTTCGGGCTGAAGACCATTAACCTCCAGAGCTCATCAATATGATGATCCGGAC 482
Db 493 ATCCACTTCGGGCTGAAGACCATTAACCTCCAGAGCTCATCAATATGATGATCCGGAC 552
QY 483 TGTATACCTTCAGCGTCTGATCAAGTTTGAACAACAGACACAGTGGCGGATCCCC 542
Db 553 TGTATACCTTCAGCGTCTGATCAAGTTTGAACAACAGACACAGTGGCGGATCCCC 612
QY 543 ATCAGCTGAGACCCAGCGCCACATCCAGAGTGTAAAGCACCCAGTGTCTCCAGCAC 602
Db 613 ATCAGCTGAGACCCAGCGCCACATCCAGAGTGTAAAGCACCCAGTGTCTCCAGCAC 672
QY 603 GGAGACAAAGCTTCGGGCTCCTGTTTGAAGTGTGTTGATCTCTCACTCTCTCTGTC 662
Db 673 GGAGACAAAGCTTCGGGCTCCTGTTTGAAGTGTGTTGATCTCTCACTCTCTCTGTC 732
QY 663 TTCTCTCTGCGCCGCTCACTCTTCAGGCTTCTGCTGCAGAACAGAGTTTGGGG 722
Db 733 TTCTCTCTGCGCCGCTCACTCTTCAGGCTTCTGCTGCAGAACAGAGTTTGGGG 792
QY 723 TTATGTGGCGGACGCGGAGCGGTCATCAGCTGTGGAGCGGCTGGAAATTTGTCAT 782
Db 793 TTATGTGGCGGACGCGGAGCGGTCATCAGCTGTGGAGCGGCTGGAAATTTGTCAT 852
QY 783 GGCTGGTACATCTGCTGCACACGAGTGTGCTACCATCTCGGCGCACCATCATGAAG 842

Db 853 GGCTGGTACATCTGCTGCTCCTCACCAGCATGTGCTCACCATCTCGGCGACCATCATGAAG 912
QY 843 ATCGGCATCGAGGCCAAGAACTTGGCAGCTACGAGCTGCGAGCATCTCTCTGGGCACC 902
Db 913 ATCGGCATCGAGGCCAAGAACTTGGCAGCTACGAGCTGCGAGCATCTCTCTGGGCACC 972
QY 903 TGAAGCTCTGCTGGTGGTGGGCGGTGATCCGCTACTGACCTTCTTCCACAACTACAAT 962
Db 973 TGAAGCTCTGCTGGTGGTGGGCGGTGATCCGCTACTGACCTTCTTCCACAACTACAAT 1032
QY 963 ATCTCTCATCGCACACTGCGGCTGGGCGCTGCCAGGTCATGCGCTTCTGCTCTGCTG 1022
Db 1033 ATCTCTCATCGCACACTGCGGCTGGGCGCTGCCAGGTCATGCGCTTCTGCTCTGCTG 1092
QY 1023 GTGTCTCATCTACCTGGGCTACTGCTTCTGCTGGCTGATCTGCTGGGCGCTTATCATGTG 1082
Db 1093 GTGTCTCATCTACCTGGGCTACTGCTTCTGCTGGCTGATCGTCTGGGCGCTTATCATGTG 1152
QY 1083 AAGTTCGCTCACTCTCCA 1101
Db 1153 AAGTTCGCTCACTCTCCA 1171

RESULT 9

AAI61022/c
ID AAI61022 standard; cDNA; 1619 BP.
XX
AC AAI61022;
XX AC
DT 22-OCT-2001 (first entry)
XX DT
DE Human polynucleotide SEQ ID NO 5011.
XX DE
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX KW
OS Homo sapiens.
XX OS
PN WO200153312-A1.
XX PN
PD 26-JUL-2001.
XX PD
PF 26-DEC-2000; 2000WO-US34263.
XX PF
PR 21-JAN-2000; 2000US-0488725.
XX PR
PR 25-APR-2000; 2000US-0552317.
XX PR
PR 09-JUL-2000; 2000US-0598042.
XX PR
PR 19-JUL-2000; 2000US-0620312.
XX PR
PR 03-AUG-2000; 2000US-0653450.
XX PR
PR 14-SEP-2000; 2000US-0662191.
XX PR
PR 19-OCT-2000; 2000US-0693036.
XX PR
PR 29-NOV-2000; 2000US-0727344.
XX PR
PA (HYSE-) HYSEQ INC.
XX PA
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
XX
DR P-PSDB; AAM41866.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Claim 1; SEQ ID NO 5011; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC

CC the encoded polypeptides (AA38642-RAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX
SQ Sequence 1619 BP; 350 A; 450 C; 518 G; 301 T; 0 other;

Query Match 93.8%; Score 1032.4; DB 22; Length 1619;
Best Local Similarity 99.8%; Pred. No. 6e-224;
Matches 1044; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY	57	GACGAGCGGATGACACCTTCGAGCTACACGCGGAGCAGCTGTACCGGCCATCTTC	116
Db	1619	GACGAGCGGATGACACCTTCGAGCTACACGCGGAGCAGCTGTACCGGCCATCTTC	1560
QY	117	CATGCTGTGACACAGTACCTGGCGTTCCTGACGTGTCACTGGGCCGATGCGTATGTC	176
Db	1559	CATGCTGTGACACAGTACCTGGCGTTCCTGACGTGTCACTGGGCCGATGCGTATGTC	1500
QY	177	CGTGTGGGGTGACCTTTGACACCAATGGCTCAGGGCTGCTCTGCGCAGCGTACTAC	236
Db	1499	CGTGTGGGGTGACCTTTGACACCAATGGCTCAGGGCTGCTCTGCGCAGCGTACTAC	1440
QY	237	CACGAGGCGACGTGGACCGCGGCAACGACACATTTCACATTGATCGATGGTGTACT	296
Db	1439	CACGAGGCGACGTGGACCGCGGCAACGACACATTTCACATTGATCGATGGTGTACT	1380
QY	297	GACTGTGATCCA-GGTGGATCCCGCGAGCGGCCCTCCGCCCCCGCAGCAGCATCTCAC	355
Db	1379	GACTGTGATCCA-GGTGGATCCCGCGAGCGGCCCTCCGCCCCCGCAGCAGCATCTCAC	1320
QY	356	CTCTTTGGAAGAGCTCCAGTTACAGAGACCTCAGCTCAAATTCACAAAGCTGTCAA	415
Db	1319	CTCTTTGGAAGAGCTCCAGTTACAGAGACCTCAGCTCAAATTCACAAAGCTGTCAA	1260
QY	416	TGTCAACATCACTTCGGCTGGAAGACCATTAACCTCCAGAGCTCATCAATATGAGAT	475
Db	1259	TGTCAACATCACTTCGGCTGGAAGACCATTAACCTCCAGAGCTCATCAATATGAGAT	1200
QY	476	CCGGAGTGTCTACCTTCAGCGCTCTGATCAAGTTTGACAAACAAAGCACAGTGGCG	535
Db	1199	CCGGAGTGTCTACCTTCAGCGCTCTGATCAAGTTTGACAAACAAAGCACAGTGGCG	1140
QY	536	GATCCCATCAGCTTGAGACCCAGGCCACATCCAGAGTGTGAAGACCCAGTGTCTT	595
Db	1139	GATCCCATCAGCTTGAGACCCAGGCCACATCCAGAGTGTGAAGACCCAGTGTCTT	1080
QY	596	CCAGCAGGAGACAAACAGCTTCGGGCTCCGTTTGGAGTGTGCTCATCTCACCTGCTC	655
Db	1079	CCAGCAGGAGACAAACAGCTTCGGGCTCCGTTTGGAGTGTGCTCATCTCACCTGCTC	1020
QY	656	CTGTCTCTCTCTCTGCGCCGCTCACTCTTCGAGGCTTCTGTCGAGAACGAGTT	715
Db	1019	CTGTCTCTCTCTCTGCGCCGCTCACTCTTCGAGGCTTCTGTCGAAACGAGTT	960
QY	716	TGTGGGTTTCATGTGGCGGACGGGACCGGTTCATCAGCTGTGGAGCGGCTGGAAT	775
Db	959	TGTGGGTTTCATGTGGCGGACGGGACCGGTTCATCAGCTGTGGAGCGGCTGGAAT	900
QY	776	TGTCAATGGCTGTACATCTCTGCTCCTCACCAGAGTGTCTCACCATCTCGGGACCAT	835
Db	899	TGTCAATGGCTGTGTACATCTCTGCTCCTCACCAGAGTGTCTCACCATCTCGGGACCAT	840

QY	836	CATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACAGCTGTGCGAGCATCTCCT	895
Db	839	CATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTGTGCGAGCATCTCCT	780
QY	896	GGCAGCTCGAGCTGCTGCTGGTGGGTGGCGTGGCGTACCGTACCTTCTTCACAA	955
Db	779	GGCAGCTCGAGCTGCTGCTGGTGGGTGGCGTGGCGTACCGTACCTTCTTCACAA	720
QY	956	CTACAATATCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTATGCGCTTCTGCTG	1015
Db	719	CTACAATATCTCATCGCCACACTGCGGGTGGCCCTGCCAGCGTATGCGCTTCTGCTG	660
QY	1016	CTCGTGGCTGTCACTACCTACCTGGGCTACTGCTTCTGTGGTGGATCGTGTGGGGCCTA	1075
Db	659	CTCGTGGCTGTCACTACCTACCTGGGCTACTGCTTCTGTGGTGGATCGTGTGGGGCCTA	600
QY	1076	TCATGTGAAGTTCGGTCACTCTCCA	1101
Db	599	TCATGTGAAGTTCGGTCACTCTCCA	574

RESULT 10

ABL35079
ID ABL35079 standard; cDNA; 1827 BP.

XX ABL35079;

XX AC AC
DT 04-APR-2002 (first entry)

DE Murine cDNA isolated from skin cells SEQ ID NO: 608.

XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
XX developmental defect; inflammatory disease; dermatological; vulnary;
XX immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
XX ss.

OS Mus sp.

XX WO200190357-A1.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-NZ00099.

XX 24-MAY-2000; 2000US-206650P.

XX 25-JUL-2000; 2000US-221232P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;

XX WPI: 2002-122020/16.

XX P-PSDB; ABB72389.

XX New polynucleotides and polypeptides encoded by the polynucleotides
XX isolated from skin cells, useful for treating skin wounds, cancers,
XX growth and developmental defects, inflammatory diseases, or for
XX modulating immune responses

XX Claim 1; Page 379-380; 466pp; English.

XX The present invention provides the protein and coding sequences of cDNAs
XX isolated from human, murine and rat skin cell libraries. The sequences
XX can be used in the development of therapeutic agents useful in the
XX treatment of skin diseases, including skin wounds, cancer, growth
XX defects, developmental defects and inflammatory diseases. The proteins
XX have important roles in the induction of hair growth, cell proliferation
XX and cell-cell interaction, in maintaining tissue integrity, in wound
XX healing and in modulating immune responses. The present sequence is a
XX cDNA of the invention.

XX Sequence 1827 BP; 392 A; 507 C; 469 G; 459 T; 0 other;

Query Match 77.3%; Score 851.4; DB 24; Length 1827;
Best Local Similarity 85.8%; Pred. No. 5.5e-183;
Matches 945; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 1 CATTCCGGGAAGAGAACACCATCGCCTTCGGACACCTCTTCCTGCTGGGCTACTCGGACG 60
DB |||||
QY 167 CATTCCGGGAAGAGAACACCATTCGCTTCGGACATCTCTTCCTGCTGGGTTACTCTGATG 226
DB |||||
QY 61 GAGCGGATGACCTTCGAGCTTACAGCGGGAGCAGCTGTACAGGCCATCTTCCATG 120
DB |||||
QY 227 GGTCTGATGACCTTTGACGCTTACACAGAGCAGCTCTACCAAGCCATCTTCTATG 286
DB |||||
QY 121 CTGTGGACCACTGCTGGCTTGGCTGAGCTGTACCTGGGCGGTATGCTATGCTCGTG 180
DB |||||
QY 287 CTGTGGACCACTGCTGCTGATCTACTACTGCTGAGATATCCCTGGGCGGTATGCTATGCTCGTG 346
DB |||||
QY 181 GTGGGGGTGACCTTGGACCAATGGCTCAGGGCTTGTCTCTGCGAGCGGTACTACCAACC 240
DB |||||
QY 347 GTGGGGGTGGGCTTGGGCCAATGGATCAGCTTTGGCTCTCTGCGAGCGGTACTACCAACC 406
DB |||||
QY 241 GAGGCCAGCTGGACCGGCCCAAGACACATTTGACATTTGATCCGATGCTGTTACTGACT 300
DB |||||
QY 407 GTGGCCATGTGGACCCAGCCCAATGATACCTTTGACATTTGATCCAAAGGTAGTCACTGACT 466
DB |||||
QY 301 GCATCAGGTGGATCCCGGAGCGGCGCCCTCGCGCCCGCCAGCGAGATCTCACCCCTCT 360
DB |||||
QY 467 GTATCCAGGTGGATCCCTCTGACAGACCGCCCTGACATCCCGCAGTGAGGACTTGGACTTCT 526
DB |||||
QY 361 TGGAAAGCAGCTCCAGTTACAAGAACTCAGCTCAAAATCCCAAGCTGCTCAATGCTCA 420
DB |||||
QY 527 TGAATGCGAGCGGAGTTACAGAACTCAGCTGAAATTTCCAGACTGATCAAGCTCA 586
DB |||||
QY 421 CCATCCACTTCCGGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATATGAGATCCCGG 480
DB |||||
QY 587 CCATCCACTTCCAGCTGAAGACCAATTAACCTCCAGAGCCTCATCAATATGAGATCCCTG 646
DB |||||
QY 481 ACTGCTATCTTCAGGCTCTGATCAGCTTTGACAAAGCAACAGTGGGCGGATCC 540
DB |||||
QY 647 ATTGTTACACTTCAGTATCTGATCAGCTTTGACAAATTAAGCGCACAGTGGGCGGATCC 706
DB |||||
QY 541 CCATCAGCTGGAGACCCAGCGCCACATCCAGAGTGTAAAGACCCAGTGTCTTCCAGC 600
DB |||||
QY 707 CCATCCGCTTGAGACCAAGACCAATCCAGAGTCAAGAGTCAACCCAGTGTCTCCAGAC 766
DB |||||
QY 601 ACGGAGACACAGCTTCCGGCTCCTGTTGACGTGGTGGTCACTCCCTCACCTGCTCCCTGT 660
DB |||||
QY 767 ATGGAGACACAGCTTCCGGCTCCTGTTGATGTTGGTGGTATCTCCACCTGCTCCCTGT 826
DB |||||
QY 661 CTTTCCTCTCTGGCGCGCTCACTCTTCGAGCTTCTGCTGCAAGACAGAGTTTGG 720
DB |||||
QY 827 CTTTCCTCTCTGGCGCGCTCACTCTTCGAGCTTCTGCTGCAAGACAGAGTTTGG 886
DB |||||
QY 721 GGTTCATGTGGCGGACGCGGCGGTGCTATCAGCTTGTGGAGCGGCTGGAAATTTGTCA 780
DB |||||
QY 887 TATTCATGTGGCGGCGGCTCGGAAATCAGCTTCTGGAAACGCTGGAGTTTGTCA 946
DB |||||
QY 781 ATGGCTGTTATCTCTGCTCTGCTCAGCAGATGCTCACCATCTCGGACCATCATGA 840
DB |||||
QY 947 ATGGCTGTTATCTCTGCTCAGCAGTACAGTGTCTCACCATCTCGGAGCTGTCTATGA 1006
DB |||||
QY 841 AGATCGGATCGAGGCAAGACTTGGCGAGCTAGCAGCTGCGAGATCTCTCTGGGCA 900
DB |||||
QY 1007 AGATTCGATTTGAGGCAAGAACTAGCCAGCTATGATGTCTGAGATTTCTCTTGGGTA 1066
DB |||||
QY 901 CTTTCAGCTGCTGCTGCTGGGCTGATCCGCTACCTGACCTTCTTCCACACTACA 960
DB |||||
QY 1067 CTTTCAGCTGCTGCTGCTGGGCTGATCCGCTACCTGACATTTTCCCAAGTACA 1126
DB |||||
QY 961 ATATCTCATCGGCACATCGGGGTGGCCCTGCCAGCGTATCGGCTTCTGCTGCTGG 1020
DB |||||
QY 1127 ACACTTGAATGCCACGTTGGAGTGGCACTGCCAGTGTGATCGGTTTCTGCTGCTGTG 1186
DB |||||

QY 1021 TGCGCTGCTACTACTGGGCTACTGCTTCTGTGCTGGAATCGCTGCTGGGCGCTTATCATG 1080
DB |||||
QY 1187 TGCGTGTCACTACTGGGCTATGCTTCTGTGCTGGAATCGCTGCTGGGCGCTTATCATG 1246
DB |||||
QY 1081 TGAAGTTCCGCTCACTCTCCA 1101
DB |||||
QY 1247 TGAAGTTCCGCTCGCTGTCCA 1267
DB |||||

RESULT 11
AAS72274
ID AAS72274 standard; cDNA; 2092 BP.
XX AAS72274;
XX DT 13-FEB-2002 (first entry)
XX DNA encoding novel human diagnostic protein #8078.
XX DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR P-PSDB; ABG08087.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity -
XX PS Claim 1; SEQ ID No 8078; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 2092 BP; 386 A; 668 C; 605 G; 433 T; 0 other;

Query Match 58.3%; Score 642.2; DB 23; Length 2092;
Best Local Similarity 83.5%; Pred. No. 1.2e-135;


```
RESULT 14
AAS89318/c
ID AAS89318 standard; cDNA; 635 BP.
XX
AC AAS89318;
XX
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #25122.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG25131.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 25122; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 635 BP; 147 A; 171 C; 210 G; 107 T; 0 other;

Query Match 30.3%; Score 334; DB 23; Length 635;
Best Local Similarity 100.0%; Pred. No. 4.7e-66;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 768 CTGGATTGTCAATGGCTGGTACATCTCTGCTCGTCACGAGGATGCTACCATCTCG 827
DB 635 CTGGATTGTCAATGGCTGGTACATCTCTGCTCGTCACGAGGATGCTACCATCTCG 576
QY 828 GGCACCATCATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACCTGTCAGC 887
DB 575 GGCACCATCATGAAGATCGGCATCGAGGCCAAGAACTTGGCGAGCTACGACCTGTCAGC 516
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QY 888 ATCTCTCTGGGCACTCGACGCTGCTGTGTGGTGGGCGTGTATCCGCTACTGACCTTC 947
DB 515 ATCTCTCTGGGCACTCGACGCTGCTGTGTGGTGGGCGTGTATCCGCTACTGACCTTC 456
QY 948 TTCCCAACTACATATCTCATCGCCACACTCGGGTGGGCGCTGCCAGCGTCAATGGC 1007
DB 455 TTCCCAACTACATATCTCATCGCCACACTCGGGTGGGCGCTGCCAGCGTCAATGGC 396
QY 1008 TTCTCTCTGCTGGTGGCTGTCTATCTTACCTGGGCTACTGCTTCTGTGGTGGATCGTGTG 1067
DB 395 TTCTCTCTGCTGGTGGCTGTCTATCTTACCTGGGCTACTGCTTCTGTGGTGGATCGTGTG 336
QY 1068 GGGCCCTATCATGTGAAGTTCGGTCACTCTCCA 1101
DB 335 GGGCCCTATCATGTGAAGTTCGGTCACTCTCCA 302

RESULT 15
AAS65931
ID AAS65931 standard; cDNA; 776 BP.
XX
AC AAS65931;
XX
DT 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #1735.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG01744.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 1735; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 635 BP; 147 A; 171 C; 210 G; 107 T; 0 other;
```

CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 776 BP; 141 A; 243 C; 248 G; 144 T; 0 other;

Query Match 25.7%; Score 282.8; DB 23; Length 776;
Best Local Similarity 99.0%; Pred. No. 1.9e-54;
Matches 295; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 CATTCGGGAAGAGAACACCATCGCCTTCGGACACCTCTTCTGCTGSGCTACTCGGACG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
401 CATTCGGGAAGAGAACACCATCGCCTTCGGACACCTCTTCTGCTGSGCTACTCGGACG 460
QY 61 GAGCGGATGACACCTTCGGAGCCTACACGCGGGAGCAGCTGTACAGGCCATCTTCCATG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
461 GAGCGGATGACACCTTCGGAGCCTACACGCGGGAGCAGCTGTACAGGCCATCTTCCATG 520
QY 121 CTGTGGACCACTACCTGGGCTTGCCTGACGTGTCACCTGGGCGGTATGCGTATGTCGGTG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
521 CTGTGGACCACTACCTGGGCTTGCCTGACGTGTCACCTGGGCGGTATGCGTATGTCGGTG 580
QY 181 GTGGGGTGACCCCTTGACCAATGGCTCAGGGCTTCTCTGCCAGCGGTACTACCAAC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
581 GTGGGGTGACCCCTTGACCAATGGCTCAGGGCTTCTCTGCCAGCGGTACTACCAAC 640
QY 241 GAGGCCACGTGACCCCGGCCACAGCACATTTGACATTGAT-CCGATGGTGGTTACTG 297
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
641 GAGGCCACGTGACCCCGGCCACAGCACATTTGACATTGATCCCGATGGTGGTTACTG 698

Search completed: October 27, 2003, 12:34:25
Job time : 368.835 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:10:42 ; Search time 4411.07 Seconds
(without alignments)
10211.014 Million cell updates/sec

Title: US-09-851-494B-2_COPY_400_1500

Perfect score: 1101
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
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- 12: gb_sy.*
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- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
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- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
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- 29: em_vi.*
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- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_man.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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4	1101	100.0	2051	9	AF287269	AF287269 Homo sapi
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6	1101	100.0	2095	6	AX280019	AX280019 Sequence
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33	103.8	9.4	579	9	AF305572S5	AF305576 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS Sequence 3 from Patent WO0177331.
DEFINITION AX280021
ACCESSION AX280021
VERSION AX280021.1 GI:16607475
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Curtis, R.A. and Silos-Santiago, I.
TITLE Human trp-like calcium channel protein-2 (tlcc-2)
JOURNAL Patent: WO 0177331-A 3 18-OCT-2001;

MILLENNIUM PHARMACEUTICALS, INC. (US)

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DEFINITION cds.
ACCESSION AF249319
VERSION AF249319.1 GI:9971787
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2004)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
Prumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Identification of the gene causing mucopolipidosis type IV
JOURNAL Nat. Genet. 26 (1), 118-123 (2000)
MEDLINE 20428196
PUBMED 10973263
REFERENCE 2 (bases 1 to 2004)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
Prumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2000) Molecular Genetics, The Weizmann Institute
of Science, P. O. Box 26, Rehovot 76100, Israel
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1 (sites)
Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2049)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:cdnal@ms.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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Qy	601	ACGAGACACAGCTTCGGCTCTGTTGACGCTGCTGCTCATCTCACCTGCTCCCTGT	660		
Db	970	ACGAGACACAGCTTCGGCTCTGTTGACGCTGCTGCTCATCTCACCTGCTCCCTGT	1029		
Qy	661	CCTTCCTCTCTGCGCCCGCTCATCTCTTCAGGCTTCTGCTGAGAACAGATTTGTGG	720		
Db	1030	CCTTCCTCTCTGCGCCCGCTCATCTCTTCAGGCTTCTGCTGAGAACAGATTTGTGG	1089		
Qy	721	GTTCATGTGGCGGAGCGGGACGGGTATCAGCTGTGGAGCGGCTGGAATTTGTCA	780		
Db	1090	GTTCATGTGGCGGAGCGGGACGGGTATCAGCTGTGGAGCGGCTGGAATTTGTCA	1149		
Qy	781	ATGGCTGTATCTCTGCTGACAGGATGTGCTCACATCTCGGGCACCATCATGA	840		
Db	1150	ATGGCTGTATCTCTGCTGACAGGATGTGCTCACATCTCGGGCACCATCATGA	1209		
Qy	841	AGATCGGATCGAGCCCAAGAACTTGGCGAGCTACGAGCTTCGACAGATCTCTCGGGCA	900		
Db	1210	AGATCGGATCGAGCCCAAGAACTTGGCGAGCTACGAGCTTCGACAGATCTCTCGGGCA	1269		

Qy	901	CCTCGACGCTGTGTGTGGTGGCGGTGATCGCGTACCTGACCTTCTTCCACAACATACA	960		
Db	1270	CCTCGACGCTGTGTGTGGTGGCGGTGATCGCGTACCTGACCTTCTTCCACAACATACA	1329		
Qy	961	ATATCTCATCGCCACACTGCGGTGCGCTGCGCCAGCGGTATGCGCTGCTGCTGCG	1020		
Db	1330	ATATCTCATCGCCACACTGCGGTGCGCTGCGCCAGCGGTATGCGCTGCTGCTGCG	1389		
Qy	1021	TGCTGTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGCGCCATCATG	1080		
Db	1390	TGCTGTCTATCTACCTGGGCTACTGCTTCTGTGGCTGGATCGTGGGCGCCATCATG	1449		
Qy	1081	TGAAGTTCCGCTCACTCTCA 1101			
Db	1450	TGAAGTTCCGCTCACTCTCA 1470			
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LOCUS		Homo sapiens mucolipin (MCOLN1) mRNA, complete cds.			
DEFINITION		Homo sapiens mucolipin (MCOLN1) mRNA, complete cds.			
ACCESSION		AF287269			
VERSION		AF287269.1 GI:9844923			
KEYWORDS		Homo sapiens (human)			
SOURCE		Homo sapiens			
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE		1 (bases 1 to 2051)			
AUTHORS		Sun, W., Goldin, E., Stahl, S., Falardeau, J.L., Kennedy, J.C., Acierno, J.S. Jr., Bove, C., Kaneski, C.R., Nagle, J., Bromley, M.C., Colman, M., Schiffmann, R. and Slaughter, S.A.			
TITLE		Mucopolidosis type IV is caused by mutations in a gene encoding a novel transient receptor potential channel			
JOURNAL		Hum. Mol. Genet. 9 (17), 2471-2478 (2000)			
MEDLINE		20485419			
PUBMED		11030752			
REFERENCE		2 (bases 1 to 2051)			
AUTHORS		Slaughter, S.A.			
TITLE		Direct Submission			
JOURNAL		Submitted (13-JUL-2000) Molecular Neurogenetics, Harvard Institute of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422, Boston, MA 02115, USA			
FEATURES		Location/Qualifiers			
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ORIGIN					
Query Match		100.0%; Score 1101; DB 9; Length 2051;			

Db	1420	TGGCTGTCTATCTACCTGGGCTACTGCTTCTGTGCTGGATCGTCTCTGTGGGCGCCCTATCATG	1479
QY	1081	TGAAGTTCGGCTCACTCTCCA	1101
Db	1480	TGAAGTTCGGCTCACTCTCCA	1500
RESULT 5			
BC005149			
LOCUS			
DEFINITION	Homo sapiens, mucolipin 1, clone MGC:3287 IMAGE:3507836, mRNA.		
ACCESSION	BC005149		
VERSION	BC005149.1 GI:13477346		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 2087)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: amadan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettman and Anuradha Madan		
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BASE COUNT	391 a	677 c	592 g 427 t
ORIGIN			

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Query Match 100.0%; Score 1101; DB 9; Length 2087;
Best Local Similarity 100.0%; Pred. No. 9.6e-195;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCGGAGAGAACACATCCCTTCGACACCTCTTCTGCTGGGTACTCGGACG 60
DB 407 CATTCCGGAGAGAACACATCCCTTCGACACCTCTTCTGCTGGGTACTCGGACG 466

QY 61 GAGCGGTGACACCTTCGACCTTACACGCGGAGAGCTGTACAGGCCATCTTCCATG 120
DB 467 GAGCGGTGACACCTTCGACCTTACACGCGGAGAGCTGTACAGGCCATCTTCCATG 526

QY 121 CTGTGGACAGTACTGCGGTTCGCTGACGCTGCTGCGGCGGTATGCGTATGTCGCTG 180
DB 527 CTGTGGACAGTACTGCGGTTCGCTGACGCTGCTGCGGCGGTATGCGTATGTCGCTG 586

QY 181 GTGGGGGTGACCTTTGACCAATGGCTCAGGCTTGTCTCTGCGAGCGGTACTACACAC 240
DB 587 GTGGGGGTGACCTTTGACCAATGGCTCAGGCTTGTCTCTGCGAGCGGTACTACACAC 646

QY 241 GAGCCACGTGGACCCCGGCCAACACATTTGACATTTGACATGTCGATGTTGTTACTGACT 300
DB 647 GAGCCACGTGGACCCCGGCCAACACATTTGACATTTGACATGTCGATGTTGTTACTGACT 706

QY 301 GCATCCAGTGGATCCCGCCGAGCGGCCCTCCGCCCCCGCCAGCGACGATCTCACCTCT 360
DB 707 GCATCCAGTGGATCCCGCCGAGCGGCCCTCCGCCCCCGCCAGCGACGATCTCACCTCT 766

QY 361 TGGAAAGCAGCTCCAGTTTACAAAGACCTCAGCTCAATTTCAAGCTGTCTCAATGTCA 420
DB 767 TGGAAAGCAGCTCCAGTTTACAAAGACCTCAGCTCAATTTCAAGCTGTCTCAATGTCA 826

QY 421 CCATCCACTCCGCTGAGACCAATTAACTCCAGAGCTTCATCAATAAGATCCCGG 480
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QY 481 ACTGCTATACCTTCAGGCTCTGATCAGTTTGACAAAGACACACAGTGGGCGGATCC 540
DB 887 ACTGCTATACCTTCAGGCTCTGATCAGTTTGACAAAGACACACAGTGGGCGGATCC 946

QY 541 CCATCAGCTCGAGACCCAGGCCACATCCAGGAGTGTAAAGACCCAGCTGTCTTCAGC 600
DB 947 CCATCAGCTCGAGACCCAGGCCACATCCAGGAGTGTAAAGACCCAGCTGTCTTCAGC 1006

QY 601 ACGGAGACACAGCTTCGCGCTCCCTGTTGACGTGGTGTATCATCTCACCTGCTCCCTGT 660
DB 1007 ACGGAGACACAGCTTCGCGCTCCCTGTTGACGTGGTGTATCATCTCACCTGCTCCCTGT 1066

QY 661 CTTTCTCTCTGCGCCGCTCAGCTCCTTCGAGGCTTCTGCTGAGAACAGATTTGTGG 720
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QY 721 GTTTCATGTGGCGGAGCGGACCGGTCATCAGCCTGTGGAGCGGTGGAAATTTGTCA 780
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QY 781 ATGCGTGTATATCTGCTGTGTCACAGGATGTGCTCACCATCTCGGCGACCATCATGA 840
DB 1187 ATGCGTGTATATCTGCTGTGTCACAGGATGTGCTCACCATCTCGGCGACCATCATGA 1246

QY 841 AGATCGGATCGAGGCCAAGACTTGGCGAGTACGAGTCTGACGCTATCTTCCAACTACA 900
DB 1247 AGATCGGATCGAGGCCAAGACTTGGCGAGTACGAGTCTGACGCTATCTTCCAACTACA 1306

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DB 1367 ATATCTCATGCCACATGCGGGTGGCCCTGCGCAGCGTATGCGCTTCTGCTGCTCG 1426

QY 1021 TGGCTGTATCTACCTTGGGCTACTGCTTCTGTGGCTGGATGCTGCTGGGCGCTTATCATG 1080
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DB 1427 TGCTGTGTCATCTACCTGGGTACTGCTTGTGGTGTGCTGCTGGGCGCTTATCATG 1486
QY 1081 TGAAGTTCGCTCACTCTCCA 1101
DB 1487 TGAAGTTCGCTCACTCTCCA 1507

RESULT 6
LOCUS AX280019 2095 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 1 from Patent WO0177331.
ACCESSION AX280019
VERSION AX280019.1 GI:16607473
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Curtis, R.A. and Silos-Santiago, I.
TITLE Human trp-like calcium channel protein-2 (tlcc-2)
JOURNAL Patent: WO 0177331-A 1 18-OCT-2001;
MILLENIUM PHARMACEUTICALS, INC. (US)
FEATURES
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ORIGIN
Query Match 100.0%; Score 1101; DB 6; Length 2095;
Best Local Similarity 100.0%; Pred. No. 9.6e-195;
Matches 1101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCCGGAGAGAACACATCCCTTCGACACCTCTTCTGCTGGGTACTCGGACG 60
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QY 61 GAGCGGTGACACCTTCGACCTTACACGCGGAGAGCTGTACAGGCCATCTTCCATG 120
DB 475 GAGCGGTGACACCTTCGACCTTACACGCGGAGAGCTGTACAGGCCATCTTCCATG 534

QY 121 CTGTGGACAGTACTGCGGTTCGCTGACGCTGCTGCGGCGGTATGCGTATGTCGCTG 180
DB 535 CTGTGGACAGTACTGCGGTTCGCTGACGCTGCTGCGGCGGTATGCGTATGTCGCTG 594

QY 181 GTGGGGGTGACCTTTGACCAATGGCTCAGGCTTGTCTCTGCGAGCGGTACTACACAC 240
DB 595 GTGGGGGTGACCTTTGACCAATGGCTCAGGCTTGTCTCTGCGAGCGGTACTACACAC 654

QY 241 GAGCCACGTGGACCCCGGCCAACACATTTGACATTTGACATGTCGATGTTGTTACTGACT 300
DB 655 GAGCCACGTGGACCCCGGCCAACACATTTGACATTTGACATGTCGATGTTGTTACTGACT 714

QY 301 GCATCCAGTGGATCCCGCCGAGCGGCCCTCCGCCCCCGCCAGCGACGATCTCACCTCT 360
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Db 715 GCATCCAGTGGATCCCGGAGCGGCGCCCTCGGCCCCCAGCGAGATCTCACCTCT 774
Qy 361 TGAAGACAGCTCCAGTTCAAGAACTCAGCTCAAAATCCCAAGCTGGTCAATGTCA 420
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Qy 421 CCATCCACTTCCGCTGAAGACCAATTAACCTCCAGAGCTCATCAATTAAGATCCGG 480
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Qy 1081 TGAAGTTCGGCTCACTTCCA 1101
Db 1495 TGAAGTTCGGCTCACTTCCA 1515

RESULT 7
LOCUS HSA293970 2037 bp mRNA linear PRI 09-NOV-2000
DEFINITION Homo sapiens mRNA for mucolipidin (ML4 gene).
ACCESSION AJ293970
VERSION AJ293970.1 GI:10129689
KEYWORDS ML4 gene; mucolipidin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bassi,M.T., Manzoni,M., Monti,E., Pizzo,M.T., Ballabio,A. and Borsani,G.
TITLE Cloning of the gene encoding a novel integral membrane protein, mucolipidin and identification of the two major founder mutations causing mucopolipidosis type IV

JOURNAL Am. J. Hum. Genet. 67 (5), 1110-1120 (2000)
MEDLINE 20489855
PUBMED 11013137
REFERENCE 2 (bases 1 to 2037)
AUTHORS Borsani,G.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Borsani G., Tigem, Via Olgettina 58, Milano, ITALY
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81..1823
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BASE COUNT 383 a 663 c 569 g 422 t

Query Match 99.9%; Score 1099.4; DB 9; Length 2037;
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Db 715 TGGAAAGCAGCTCCAGTTACAAGAACTCAGCTCAAAATCCCAAGCTGGTCAAATGTCA 774
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Db 775 CCATCCACTTCCGCTGAAGACCAATTAACCTCCAGAGCTCATCAATTAAGATCCCGG 834

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Qy 601 ACGGAGAAACAGCTTCGGGCTCTGTTTGAAGTGGTGTCTCACTCCTCCTCCTGT 660
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Db 1015 CTTCTCCTCTGCGCGGCTCACTCCTCCTGAGGCTTCTGTCAGAACAGTGTGG 1074
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RESULT 8
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LOCUS Sequence 50 from Patent WO0112662.
DEFINITION AX083508
ACCESSION AX083508
VERSION AX083508.1 GI:13185318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lal, P., Yue, H., Tang, Y.T., Bandman, O., Burford, N., Azimzai, Y.,
Baughn, M.R., Lu, D.A. and Patterson, C.
Membrane associated proteins
Patent: WO 0112662-A 50 22-FEB-2001;
Incyte Genomics, Inc. (US)
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Location/Qualifiers
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RESULT 9

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LOCUS Homo sapiens mRNA for mucolipidin, short form (ML4 gene).

DEFINITION

ACCESSION AJ293659

VERSION AJ293659.1 GI:10045134

KEYWORDS alternative splicing; ML4 gene; mucolipidin.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Bassi,M.T., Manzoni,M., Monti,E., Pizzo,M.T., Ballabio,A. and Borsani,G.

TITLE Cloning of the gene encoding a novel integral membrane protein, mucolipidin-and identification of the two major founder mutations causing mucopolidosis type IV

JOURNAL Am. J. Hum. Genet. 67 (5), 1110-1120 (2000)

MEDLINE 20489855

PUBMED 11013137

REFERENCE 2 (bases 1 to 2272)

AUTHORS Borsani,G.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-2000) Borsani G., Telethon Institute of Genetics and Medicine - TIGEM, Via Olgettina 58, 20132 Milano, ITALY

REMARK Revised by author

FEATURES

Location/Qualifiers

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BASE COUNT 422 a 748 c 647 g 455 t

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Qy 121 CTGTGGACCAAGTACTCTGGCGTTCCTCACTGCTGCTGCGGCGGATGCGGTATGTCCTGTG 180

Db 475 CTGTGGACCAAGTACTCTGGCGTTCCTCACTGCTGCTGCGGCGGATGCGGTATGTCCTGTG 534

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Db 715 TGGAAACGACGCTCCAGTTACAAGAACTCAGCTCAAAATTCACAAAGTACTGCTGCTCA 774

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BC005651
LOCUS
DEFINITION
Mus musculus mucolipin 1, mRNA (cdna clone MGC:7172 IMAGE:3257440), complete cds.
ACCESSION
BC005651
VERSION
BC005651.1
KEYWORDS
GI:13542918
SOURCE
MGC.
ORGANISM
Mus musculus (house mouse)
REFERENCE
Mammalia; Eutheria; Chordata; Sciuromorphia; Muridae; Murinae; Mus.
1 (bases 1 to 2039)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullighy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
PUBMED
12477932
2 (bases 1 to 2039)
Strausberg, R.
Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunsatne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louisse, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 6 Row: c Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.
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RESULT 13
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DEFINITION Mus musculus mucolipin-3 (Mcoln3) mRNA, complete cds.
ACCESSION AF475086
VERSION AF475086.1 GI:19072755
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1712)
Falardeau, J.L., Kennedy, J.C., Acierno, J.S. and Slaugenaupt, S.A.
Cloning of the mouse Mcoln3 gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1712)
Falardeau, J.L., Kennedy, J.C., Acierno, J.S. and Slaugenaupt, S.A.
Direct Submission
JOURNAL Submitted (24-JAN-2002) Molecular Neurogenetics, Harvard Institute
of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422,
Boston, MA 02115, USA
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454 a 412 c 402 g 444 t

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RESULT 14
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LOCUS Homo sapiens mucolipin-3 (MCOLN3) mRNA, complete cds.
DEFINITION AF475085
ACCESSION AF475085
VERSION AF475085.1 GI:19072753
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1900)
AUTHORS Falardeau, J.L., Kennedy, J.C., Acierno, J.S. and Slaugenaupt, S.A.
TITLE Cloning of the MCOLN3 gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1900)
AUTHORS Falardeau, J.L., Kennedy, J.C., Acierno, J.S. and Slaugenaupt, S.A.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-2002) Molecular Neurogenetics, Harvard Institute
of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422,
Boston, MA 02115, USA
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Db 1303 GCTGTGAGCTATGATTTACTTAGGTTACTGCTTCTGTGATGATGATGCTGCTGGGGCCT 1362
Qy 1075 ATCATGTGAAGTTCGGCTCACTCTCCA 1101
Db 1363 ACCATGACAAGTTTCGTTCTCTGAAACA 1389

RESULT 15
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LOCUS BD156806
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD156806
VERSION BD156806.1 GI:27862564
KEYWORDS JP 2002191363-A/11649.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1762)
AUTHORS Ota, T., Isozaki, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 11649 09-JUL-2002;
HELIIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/11649
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOZAKI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/00, C12P21/02, C12P21/08, G06F17/30, C12N15/00, C12N5/00, C12N5/00 CC
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Best Local Similarity 57.6%; Pred. No. 1.5e-38;
Matches 525; Conservative 0; Mismatches 357; Indels 30; Gaps 2;
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Job time : 4421.07 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 12:19:17 ; Search time 63.6775 Seconds

(without alignments)

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Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	142.4	70.8	2052	11	US-09-969-880A-50
5	142.4	70.8	2054	9	US-09-820-893-26
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7	142.4	70.8	2095	13	US-10-103-458-1
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10	121.4	60.4	463	11	US-09-918-995-27041
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12	52.4	26.1	1912	11	US-09-796-753-161
13	50.4	25.1	207	9	US-09-864-761-28893
14	42	20.9	668	11	US-09-764-872-676
15	41.4	20.6	1677	12	US-10-305-810-4
16	41.4	20.6	1677	12	US-10-114-153-21

C 17	41.2	20.5	1520	11	US-09-992-600A-107	Sequence 107, App
C 18	41.2	20.5	1520	11	US-09-924-340-107	Sequence 107, App
C 19	41.2	20.5	1520	12	US-09-992-095B-107	Sequence 107, App
C 20	41.2	20.5	1520	12	US-10-154-678-107	Sequence 107, App
C 21	41.2	20.5	1520	12	US-09-999-570-107	Sequence 107, App
C 22	41.2	20.5	1520	14	US-10-000-489-107	Sequence 107, App
C 23	41.2	20.5	1520	14	US-10-000-986-107	Sequence 107, App
C 24	41.2	20.5	1528	11	US-09-746-783-183	Sequence 183, App
C 25	41.2	20.5	1554	14	US-10-037-270-802	Sequence 802, App
C 26	40.6	20.2	1671	12	US-10-114-153-23	Sequence 23, Appl
C 27	40.6	20.2	2067	12	US-10-114-153-27	Sequence 27, Appl
C 28	40.6	20.2	2130	12	US-10-114-153-25	Sequence 25, Appl
C 29	40.2	20.0	594	12	US-10-140-472-10	Sequence 10, Appl
C 30	40.2	20.0	594	12	US-10-141-761-10	Sequence 10, Appl
C 31	40.2	20.0	594	12	US-10-142-885-10	Sequence 10, Appl
C 32	40.2	20.0	594	12	US-10-158-790-10	Sequence 10, Appl
C 33	40.2	20.0	594	14	US-10-123-155-10	Sequence 10, Appl
C 34	40.2	20.0	594	15	US-10-146-731-10	Sequence 10, Appl
C 35	40	19.9	1470	14	US-10-156-761-5816	Sequence 5816, Ap
C 36	40	19.9	9025608	14	US-10-156-761-1	Sequence 1, Appl
C 37	37.2	18.5	1926	12	US-10-294-804-3	Sequence 3, Appl
C 38	37.2	18.5	8705	14	US-10-291-230-14	Sequence 14, Appl
C 39	37.2	18.5	8705	14	US-10-291-249-14	Sequence 14, Appl
C 40	37.2	18.5	9600	12	US-10-278-751-1	Sequence 1, Appl
C 41	37.2	18.5	10233	12	US-10-050-898-283	Sequence 283, App
C 42	37.2	18.5	10285	12	US-10-050-908-283	Sequence 283, App
C 43	36	17.9	1506	14	US-10-156-761-5159	Sequence 5159, App
C 44	35.2	17.5	1882	14	US-10-037-270-427	Sequence 427, App
C 45	34.4	17.1	1224	12	US-09-953-348-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-828-466-3
; Sequence 3, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-12SCP
; CURRENT APPLICATION NUMBER: US/09/828,466
; CURRENT FILING DATE: 2001-04-06
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1740)
US-09-828-466-3

Qy	58	GCAGTTCCGCTCACTCTCCATGGTGTCTGAGTGCCTTCTCGCTCATCAATGGGACGA	117
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Qy	118	CATGTTGTGACGTTCCGCCCATCGAGGCGAGAGCCGCGAGAGCCCTGGTGGCT	177
Db	1416	CATGTTGTGACGTTCCGCCCATCGAGGCGAGAGCCGCGAGAGCCCTGGTGGCT	1475
Qy	178	CTTCTCCAGCTCTACTTCTTCTC	201
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; LENGTH: 207
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013291.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.46
; OTHER INFORMATION: SWISSPROT HIT: Q13563, EVALUAE 6.00e-03
; OTHER INFORMATION: EST HUMAN HIT: N41861.1, EVALUAE 5.00e-08
; OTHER INFORMATION: NT HIT: g18922819, EVALUAE 1.00e-113
US-09-864-761-28893

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Best Local Similarity 75.0%; Pred. No. 1.4e-05;
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; Sequence 676, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 676
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-676

Query Match 20.9%; Score 42; DB 11; Length 668;

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Best Local Similarity 60.7%; Pred. No. 0.0046;
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DB 205 TGATGACATGTTTGCAACCTTTGCCAAATCCAGCAGAG-----AGCATTTTGGT 255

QY 172 GTGGCTCTTCTCCAGCTCTACCTTTACTC 201
DB 256 GTGGCTGTTCACTGCTGCTGATTTATTC 285

RESULT 15
US-10-305-810-4
; Sequence 4, Application US/10305810
; Publication No. US20030176385A1
; GENERAL INFORMATION:
; APPLICANT: Ju, Jingfang
; APPLICANT: Huang, Chunli
; APPLICANT: Zhong, Haihong
; APPLICANT: Simons, Jan Fredrik
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Chant, John S.
; APPLICANT: Peyman, John A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN EXPRESSION
; FILE REFERENCE: 21402-501
; CURRENT APPLICATION NUMBER: US/10/305,810
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/334,148
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/336,572
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/625,634
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/192,838
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/194,256
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/970,813
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/182,637
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/240,316
; PRIOR FILING DATE: 2000-10-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 4
; LENGTH: 1677
; TYPE: DNA
; ORGANISM: Ion Transport Channel (Ag 1987)
US-10-305-810-4

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Best Local Similarity 61.5%; Pred. No. 0.0074;
Matches 88; Conservative 0; Mismatches 46; Indels 9; Gaps 1;

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DB 1261 CAGTTTGAANAATCTGAACACAGTTGCTGAGTGTCTGTTTCTCTGCTCAACGCTGATGAC 1320

QY 119 ATGTTTGTGACGTTTCGCCCATGTCAGCGCCGACAGCGCGCAGAGCTGTGTGGCTC 178

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Db 1321 ATGTTGCAACCTTTGCCCAATCCAGCAGAG-----AGCACTTGGTGGCTG 1371

Oy 179 TTCTCCAGCTCTACCTTTACTC 201

Db 1372 TTCAGTCGTCTGTATTATATTC 1394

Search completed: October 27, 2003, 18:02:14
Job time : 75.6775 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:28:31 ; Search time 65.3268 Seconds
(without alignments)
8305.735 Million cell updates/sec

Title: US-09-851-494B-1_COPY_9000_9200

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	11365	22	AAK73827 Human immune/haema
2	201	100.0	20046	22	AAK73826 Human immune/haema
3	143.4	71.3	3371	23	AA889322 DNA encoding novel
4	143.2	71.2	318	23	AA889310 DNA encoding novel
5	143.2	71.2	2092	23	AA872274 DNA encoding novel
6	142.4	70.8	1740	24	ABL40755 Human TRCC-2 prote
7	142.4	70.8	1740	24	AA171700 Human TRP-like cal
8	142.4	70.8	1741	22	AA159236 Human polynucleoti

9	142.4	70.8	2052	22	AAF81753 Human membrane ass
10	142.4	70.8	2092	24	ABL90358 Human polynucleoti
11	142.4	70.8	2094	21	AAA39067 Human secreted pro
12	142.4	70.8	2095	24	ABL40754 Human TLCC-2 prote
13	142.4	70.8	2095	24	AA171599 Human TRP-like cal
14	140.8	70.0	635	23	AA889318 DNA encoding novel
15	131.4	65.4	1619	22	AA161022 Human polynucleoti
16	122.4	60.9	1827	24	Murine cDNA isolat
17	54	26.9	531	22	AAK08799 Human brain expres
18	54	26.9	531	22	AA140407 Probe #9093 used t
19	54	26.9	531	22	AA834459 Human liver single
20	52.4	26.1	1762	22	AAH14814 Human cDNA sequenc
21	52.4	26.1	1912	22	AAK01697 Human TANGO 480 cD
22	50.4	25.1	207	22	AAK21491 Human brain expres
23	50.4	25.1	207	22	AA153486 Probe #22172 used
24	50.4	25.1	207	23	ABS47387 Human liver single
25	46.4	23.1	499	23	AA872273 DNA encoding novel
26	42	20.9	668	22	AA539779 Genomic sequence #
27	42	20.9	668	22	AAK90132 Human digestive sy
28	41.4	20.6	1677	25	ABX56271 Human NOV9a CG9070
29	41.2	20.5	1468	21	AAA95496 Hela cell library
30	41.2	20.5	1520	25	ACC51113 Human JNK3-binding
31	41.2	20.5	1528	20	AAK35555 Secreted protein c
32	41.2	20.5	1554	22	AA158910 Human polynucleoti
33	41.2	20.5	1749	22	AA160696 Human secreted pro
34	40.6	20.2	492	22	ABA08523 Human NOV9b CG9070
35	40.6	20.2	1671	25	ABX56272 Human NOV9d CG9070
36	40.6	20.2	2067	25	ABX56274 Human NOV9c CG9070
37	40.6	20.2	2130	25	ABX56273 Drosophila melanog
38	39.6	19.7	2194	23	ABL29717 Drosophila melanog
39	39.6	19.7	5035	23	ABL29716 Nucleotide sequenc
40	37.2	18.5	799	19	AAV55831 Epstein Barr Virus
41	37.2	18.5	1925	20	AAK90924 Epstein Barr Virus
42	37.2	18.5	1926	21	AA450254 EBV tethering prot
43	37.2	18.5	1926	21	AAJF82902 Nucleotide sequenc
44	37.2	18.5	2580	21	AA475454 Epstein-Barr virus
45	37.2	18.5	2580	24	AA164275

ALIGNMENTS

RESULT 1

AAK73827

ID AAK73827 standard; DNA; 11365 Bp.

XX AAK73827;

AC AAK73827;

XX 07-NOV-2001 (first entry)

DT Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

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DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

DE Human immune/haematopoietic antigen genomic sequence

CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 11365 BP; 2407 A; 3320 C; 3153 G; 2485 T; 0 other;

Query Match 100.0%; Score 201; DB 22; Length 11365;
 Best Local Similarity 100.0%; Pred. No. 6.3e-44;
 Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCCAGCCCCCGGTTCTCGCCATGCCCTTGCTCCCTGACCGCGCCCTCTGGCA 60
 Db 7581 CCCAGCCCCCGGTTCTCGCCATGCCCTTGCTCCCTGACCGCGCCCTCTGGCA 7640
 Qy 61 GTTCGGTCACTCCATGGTGTGAGTGGCTGTTCGCTCATCAATGGGGACGACAT 120
 Db 7641 GTTCGGTCACTCCATGGTGTGAGTGGCTGTTCGCTCATCAATGGGGACGACAT 7700
 Qy 121 GTTTGTGACGTTCCCGCCATGCCAGCGCCAGCGCGCGAGCGCTGTGGCTCTT 180
 Db 7701 GTTTGTGACGTTCCCGCCATGCCAGCGCCAGCGCGCGAGCGCTGTGGCTCTT 7760
 Qy 181 CTCCAGCTCTACCTTTACTC 201
 Db 7761 CTCCAGCTCTACCTTTACTC 7781

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 ID AAK73826 standard; DNA; 20046 BP.
 XX
 AC AAK73826;
 XX
 DT 07-NOV-2001 (first entry)
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28638.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cyostatic; gene therapy; vaccine; metastasis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WC200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01354.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
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 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
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 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218230.
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 PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.
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 PR 14-AUG-2000; 2000US-0225214.
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 PR 08-SEP-2000; 2000US-0232080.
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 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
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 PR 14-SEP-2000; 2000US-0232399.
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 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 21-SEP-2000; 2000US-0234223.
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 PR 25-SEP-2000; 2000US-0234597.
 PR 25-SEP-2000; 2000US-0234598.
 PR 25-SEP-2000; 2000US-0234599.
 PR 27-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
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 PR 29-SEP-2000; 2000US-0236368.
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 PR 02-OCT-2000; 2000US-0237038.
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 PR 02-OCT-2000; 2000US-0237040.
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 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
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 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244517.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.

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CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
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SQ Sequence 20046 BP; 4133 A; 5821 C; 5659 G; 4433 T; 0 other;

Query Match          100.0%; Score 201; DB 22; Length 20046;
Best Local Similarity 100.0%; Pred. No. 6.9e-44;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGCCCCCGGTTCTCTGGCCATCGCTTGGCTTCCTCTGACCCGCGCCGCTCTGGCA 60
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QY 61 GTTCGGCTCACTCTCCATNGGTCTCTGAGTGCTCTGTTCGCTCATCAATGGGACGACAT 120
Db 7661 GTTCGGCTCACTCTCCATNGGTCTCTGAGTGCTCTGTTCGCTCATCAATGGGACGACAT 7720

QY 121 GTTTGTGAGCTTCGGCGCCATCGACGCGCAGCAGGCGCCGACGAGCCTCTGTGTGGCTCTT 180
Db 7721 GTTTGTGAGCTTCGGCGCCATCGACGCGCAGCAGGCGCCGACGAGCCTCTGTGTGGCTCTT 7780

QY 181 CTCCAGAGCTCTACCTTTACTC 201
Db 7781 CTCCAGAGCTCTACCTTTACTC 7801

RESULT 3
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XX AAS89322;
XX AC
XX XX
XX DT
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #25126.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG25135.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1; SEQ ID No 25126; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX CC. (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX

```

CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AA864157-AA894564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 3371 BP; 842 A; 918 C; 907 G; 704 T; 0 other;

Query Match 71.3%; Score 143.4; DB 23; Length 3371;
 Best Local Similarity 96.1%; Pred. No. 1e-28;
 Matches 147; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 49 GCCCCTCTGCAGTTCGGCTCACTCTCCATGGTGTCTGAGTGCTGTCTCGCTCATCAA 108
 DB 585 GCGCCACACAGATGTTCCGCTCACTCTCCATGGTGTCTGAGTGCTGTCTCGCTCATCAA 644
 QY 109 TGGGAGCAGCATGTTGTGAGCTTGGCGGCATCGAGCGCAGCAGGCGCGCAGCAGCCT 168
 DB 645 TGGGAGCAGCATGTTGTGAGCTTGGCGGCATCGAGCGCAGCAGGCGCGCAGCAGCCT 704
 QY 169 GGTGTGGCTTCTCCAGCTTACCTTTACTC 201
 DB 705 GGTGTGGCTTCTCCAGCTTACCTTTACTC 737

RESULT 4
 AAS89310
 ID AAS89310 standard; cDNA; 318 BP.
 XX
 AC AAS89310;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #25114.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG25123.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1; SEQ ID No 25114; 103pp; English.

XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (II) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AA864157-AA894564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 318 BP; 52 A; 109 C; 76 G; 81 T; 0 other;
 Query Match 71.2%; Score 143.2; DB 23; Length 318;
 Best Local Similarity 92.1%; Pred. No. 7.7e-29;
 Matches 151; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 38 CTGACCCCGCGCCCTCTGGCAGTTCGCTCACTCTCCATGGTGTCTGAGTGCTGTCTCGCTTTC 97
 DB 79 CTGACCTTCTTCCACAACACTACAATTTCCGCTCACTCTCCATGGTGTCTGAGTGCTTTC 138
 QY 98 TCGCTCATCAATGGGAGCAGCATGTTGTGAGCTTGGCGGCATCGAGCGCAGCAGGCGGC 157
 DB 139 TCGCTCATCAATGGGAGCAGCATGTTGTGAGCTTGGCGGCATCGAGCGCAGCAGGCGGC 198
 QY 158 CGCAGCAGCTGTGTGGCTTCTTCCAGCTTACCTTTACTC 201
 DB 199 CGCAGCAGCTGTGTGGCTTCTTCCAGCTTACCTTTACTC 242

RESULT 5
 AAS72274
 ID AAS72274 standard; cDNA; 2092 BP.
 XX
 AC AAS72274;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #8078.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
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 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
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 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG08087.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX PS Claim 1; SEQ ID No 8078; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX CC and gene mapping, and in recombinant production of (II). The

XX CC polynucleotides are also used in diagnostics as expressed sequence tags

XX CC for identifying expressed genes. (I) is useful in gene therapy techniques

XX CC to restore normal activity of (II) or to treat disease states involving

XX CC (II). (II) is useful for generating antibodies against it, detecting or

XX CC quantitating a polypeptide in tissue, as molecular weight markers and as

XX CC a food supplement. (II) and its binding partners are useful in medical

XX CC imaging of sites expressing (II). (I) and (II) are useful for treating

XX CC disorders involving aberrant protein expression or biological activity.

XX CC The polypeptide and polynucleotide sequences have applications in

XX CC diagnostics, forensics, gene mapping, identification of mutations

XX CC responsible for genetic disorders or other traits to assess biodiversity

XX CC and to produce other types of data and products dependent on DNA and

XX CC amino acid sequences. AAS64197-AAS94564 represent novel human

XX CC diagnostic coding sequences of the invention.

XX CC Note: The sequence data for this patent did not appear in the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 2092 BP; 386 A; 668 C; 605 G; 433 T; 0 other;

Query Match 71.2%; Score 143.2; DB 23; Length 2092;

Best Local Similarity 92.1%; Pred. No. 1.1e-28;

Matches 151; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 38 CTGACCCCGCCGCTCTGGGAGTTCCGCTCACTCTCCATGTTGTCAGTGCCTGTC 97

DB 1460 CTGACCTTCTTCACAACTACAAATTTCCGCTCACTCTCCATGTTGTCAGTGCCTGTC 1519

QY 98 TCCTCATCAATGGGAGGACATGTTGTGAGCTTCGCGCCATGCGAGCGGAGGAGG 157

DB 1520 TCCTCATCAATGGGAGGACATGTTGTGAGCTTCGCGCCATGCGAGCGGAGGAGG 1579

QY 158 CGAGAGAGCTGTGTGGCTTCTTCTCCAGCTCTACCTTTACTC 201

DB 1580 CGCAGAGAGCTGTGTGGCTTCTTCTCCAGCTCTACCTTTACTC 1623

RESULT 6

ABL40755

ID ABL40755 standard; cDNA; 1740 BP.

XX AC ABL40755;

XX DT 03-JUL-2002 (first entry)

XX DE Human TLCC-2 protein coding sequence.

XX KW Transient receptor potential like calcium channel; TRP; TLCC-2; human;

XX KW neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;

XX KW cerebroprotective; anxiolytic; antitonic; anticonvulsant; gene therapy;

XX KW calcium signaling; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 1..1740

XX FT /*tag= a

XX FT /product= "TLCC-2"

XX FT /note= "transient receptor potential-like calcium

XX FT channel"

XX US2002035056-A1.

XX PN 21-MAR-2002.

XX PD 06-APR-2001; 2001US-0828466.

XX PR 07-APR-2000; 2000US-0544797.

XX FA (CURTIS/ CURTIS R A J.

XX SILO/ SILOS-SANTIAGO I.

XX PI Curtis RAJ, Silos-Santiago I;

XX DR WPI: 2002-338931/37.

XX DR P-PSDB; ABB07816.

XX PT New nucleic acid designated TLCC-2 encodes a transient receptor

XX PT potential-like calcium channel and is useful to diagnose and treat pain

XX PT disorders and central nervous system neurodegenerative and neurological

XX PT disorders -

XX PS Claim 1; Fig 1A-B; 70pp; English.

XX CC The invention relates to a novel transient receptor potential (TRP)-like

XX CC calcium channel, designated TLCC-2 and polynucleotides encoding the

XX CC TLCC-2. TLCC-2 can be expressed by standard recombinant methodology. The

XX CC TLCC-2 polypeptide, polynucleotides and modulators are useful for

XX CC treating central nervous system disorders such as neurodegenerative

XX CC disorders for example Alzheimer's disease, Parkinson's disease, multiple

XX CC sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy,

XX CC epilepsy, Creutzfeldt-Jakob disease, AIDS-related dementia, familial

XX CC infantile convulsions, paroxysmal choreoathetosis, psychiatric disorders

XX CC such as depression, anxiety, schizophrenia, psychoses, mania or phobic

XX CC disorders, learning or memory disorders such as amnesia, age-related

XX CC memory loss, or a neurological disorder such as migraine. The molecules

XX CC are also useful to treat a pain disorder. The present sequence represents

XX CC the coding sequence of the human TLCC-2 polypeptide.

XX SQ Sequence 1740 BP; 319 A; 578 C; 475 G; 368 T; 0 other;

Query Match 70.8%; Score 142.4; DB 24; Length 1740;

Best Local Similarity 99.3%; Pred. No. 1.7e-28;

Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GCAGTTCCGCTCACTCTCCATGTTGTCAGTGCCTGTTCTCGCTCATCATGGGAGCA 117

DB 1356 GAAGTTCCGCTCACTCTCCATGTTGTCAGTGCCTGTTCTCGCTCATCATGGGAGCA 1415

QY 118 CATGTTTGTCAGCTTCGCGCCATGCGAGCGGAGGCGGCGGAGCTGGTGTGGCT 177

DB 1416 CATGTTTGTCAGCTTCGCGCCATGCGAGCGGAGGCGGCGGAGCTGGTGTGGCT 1475

QY 178 CTCTCCAGCTCTACCTTTACTC 201

DB 1476 CTCTCCAGCTCTACCTTTACTC 1499

RESULT 7

AAI71700

ID AAI71700 standard; cDNA; 1740 BP.

XX AC AAI71700;

XX DT 29-JAN-2002 (first entry)

XX DE Human TRP-like calcium channel TLCC-2 coding sequence #2.

XX KW Human; TLCC-2; TRP-like calcium channel; membrane excitability;

XX KW nociception; nootropic; neuroprotective; antiparkinsonian; cytostatic;

XX KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;

XX KW Parkinson's disease; Huntington's disease; multiple sclerosis;

XX KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;

XX KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 1..1740

DE Human membrane associated protein MEMAP-13 encoding cDNA.

XX Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
 KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
 KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
 KW autoimmune disorder; inflammatory disorder; neurological disorder;
 KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
 KW epilepsy; diarrhoea; ss.

XX Homo sapiens.

XX WO200112662-A2.

XX 22-FEB-2001.

XX 14-AUG-2000; 2000WO-US22315.

XX 17-AUG-1999; 99US-0149641.

PR 09-NOV-1999; 99US-0164203.

XX (INCY-) INCYTE GENOMICS INC.

XX Lal P. Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
 PI Baughn MR, Lu DAM, Patterson C;
 XX WPI; 2001-168860/17.
 DR P-PSDB; AAB74707.

XX Isolated polypeptide with a human membrane associated protein sequence
 is useful for the diagnosis, prevention and treatment of cell
 proliferative, autoimmune/inflammatory, neurological and
 gastrointestinal disorders -

XX Claim 5; Page 157-158; 173pp; English.

XX AAF81741 to AAF81777 encode the human membrane associated proteins
 (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
 antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
 antiarteriosclerotic activities, which can be used in gene therapy.
 CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
 CC associated with decreased expression of functional MEMAP and antagonists
 CC of MEMAP are used to treat a disease or condition associated with
 CC overexpression of functional MEMAP. These disorders include cell
 CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
 CC disorders. The MEMAP polynucleotides and proteins are also used for the
 CC diagnosis of these disorders. Specific examples of these disorders
 CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
 CC MEMAP proteins can be used to screen for compounds which specifically
 CC bind MEMAP including antibodies, oligonucleotides, proteins and small
 CC molecules. MEMAP polynucleotides can be used to prepare transgenic
 CC animals which can be studied to provide information concerning human
 CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
 CC detection of MEMAP protein and can be used as antagonists to treat or
 CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
 CC can be delivered to target cells with genetic abnormalities with respect
 CC to the expression of MEMAP to treat or prevent a disorder associated
 CC with MEMAP.

XX Sequence 2052 BP; 375 A; 670 C; 582 G; 425 T; 0 other;

Query Match 70.8%; Score 142.4; DB 22; Length 2052;
 Best Local Similarity 99.3%; Pred. No. 1.8e-28;
 Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GCAGTTCGCTCACTCTCCATGGTGTCTGAGTGTCTTCGCTCATCAATGGGACGA 117
 DB 1463 GAAATTCGCTCACTCTCCATGGTGTCTGAGTGTCTTCGCTCATCAATGGGACGA 1522

QY 118 CATGTTTGTGAGCTTCGCGCCGATGCGAGCGGCAGCGAGCGCTGTGTGGCT 177
 DB 1523 CATGTTTGTGAGCTTCGCGCCGATGCGAGCGGCAGCGAGCGCTGTGTGGCT 1582

QY 178 CTCTCCAGCTCTACTTTTACTC 201

DB 1583 CTCTCCAGCTCTACTTTTACTC 1606

RESULT 10
 ABL90358
 ID ABL90358 standard; cDNA; 2092 BP.
 XX AC ABL90358;
 XX 24-MAY-2002 (first entry)
 XX Human polynucleotide SEQ ID NO 920.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss.

XX Homo sapiens.

XX WO2001190304-A2.

XX 29-NOV-2001.

XX 18-MAY-2001; 2001WO-US16450.

XX 19-MAY-2000; 2000US-205515P.
 (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;
 XX WPI; 2002-122018/16.
 XX P-PSDB; ABB89949.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders -

XX Claim 4; SEQ ID NO 920; 2081pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL89449-ABL90833) and proteins
 (AB893040-AB890444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC epilepsy; and (f) neurological diseases e.g. cerebral anoxia and
 CC and parasitic infections.

XX Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2092 BP; 399 A; 676 C; 590 G; 425 T; 2 other;

Query Match 70.8%; Score 142.4; DB 24; Length 2092;
 Best Local Similarity 99.3%; Pred. No. 1.8e-28;
 Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GCAGTTCGCTCACTCTCCATGGTGTCTGAGTGTCTTCGCTCATCAATGGGACGA 117
 DB 1463 GAAATTCGCTCACTCTCCATGGTGTCTGAGTGTCTTCGCTCATCAATGGGACGA 1522

QY 118 CATGTTTGAGCTTCGGCGCATGCGGCGAGCGGCGGCGAGCGCTGGTGGCT 177
 DB 1523 CAAGTTTGAGCTTCGGCGCATGCGGCGAGCGGCGGCGAGCGCTGGTGGCT 1582
 QY 178 CTTCTCCAGCTCTACCTTTACTC 201
 DB 1583 CTTCTCCAGCTCTACCTTTACTC 1606

RESULT 11

AAA39067

ID AAA39067 standard; cDNA; 2094 BP.

XX AC

XX AAA39067;

XX DT

XX 30-AUG-2000 (first entry)

XX DE

XX Human secreted protein gene 16 SEQ ID NO:26.

XX KW

XX Human; secreted protein; cytostatic; anti-proliferative; vulnery;

XX immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis;

XX hyperproliferative disorder; infectious disease; tissue regeneration;

XX screening; food additive; preservative; wound healing;

XX hyper-vascular disease; ss.

XX OS

XX Homo sapiens.

XX PN

XX WO200017222-A1.

XX XX

XX 30-MAR-2000.

XX PF

XX 22-SEP-1999; 99WO-US22012.

XX PR

XX 23-SEP-1998; 98US-0101546.

XX PR

XX 02-OCT-1998; 98US-0102895.

XX XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX PA

XX Ruben SM, Rosen CA, Duan RD, Shi Y, Lafleur DW, Young PE, Ni J;

XX PI

XX Komatsoulis G, Endress GA, Soppet DR;

XX XX

XX WPI: 2000-283538/24.

XX DR

XX P-PSDB; AAB08906.

XX XX

XX Human secreted proteins and coding sequences useful in diagnostic and

XX therapeutic methods for disorders such as immune system or

XX proliferative disorders, related to the proteins

XX PS

XX Claim 1; Page 331-332; 416pp; English.

XX CC

XX The polynucleotide sequences given in AAA39052 to AAA39088 encode the

XX human secreted proteins given in AAB08891 to AAB08984. The human secreted

XX proteins can have activities based on the tissues and cells they are

XX expressed in. Examples of the activities are: cytostatic;

XX anti-proliferative; immunosuppressive; antibacterial; and vulnery. The

XX secreted proteins and their related polynucleotide sequences are useful

XX for diagnostic and therapeutic methods useful for diagnosing and treating

XX disorders related to the secreted proteins. The proteins, and

XX polynucleotide sequences may be useful for treating disorders of the

XX immune system, hyperproliferative disorders, infectious disease,

XX regeneration of tissues, for chemotaxis and for screening molecules

XX bind to the proteins. The proteins or polynucleotide sequences may be

XX used as food additives or preservatives, to increase or decrease storage

XX capabilities, fat content, lipid, protein, carbohydrate, vitamins,

XX minerals, co-factors or other nutritional components. Agonists or

XX antagonists of the proteins may be used to prevent scar tissue growth

XX during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051

XX and AAB08890 are sequences used in the exemplification of the present

XX invention.

XX XX

XX Sequence 2094 BP; 400 A; 673 C; 589 G; 426 T; 6 other;

XX SQ

XX Query Match

XX 70.88; Score 142.4; DB 21; Length 2094;

Best Local Similarity 99.3%; Pred. No. 1.8e-28;
 Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GCAGTTCCTCCCTCACTCTCCATGCTCTGAGTGCCTGTTCTCGCTCATCAATGGGACGA 117
 DB 1463 GAAGTTCCTCCCTCACTCTCCATGCTCTGAGTGCCTGTTCTCGCTCATCAATGGGACGA 1522
 QY 118 CATGTTTGAGCTTCGGCGCATGCGGCGAGCGGCGGCGAGCGCTGGTGGCT 177
 DB 1523 CATGTTTGAGCTTCGGCGCATGCGGCGAGCGGCGGCGAGCGCTGGTGGCT 1582
 QY 178 CTTCTCCAGCTCTACCTTTACTC 201
 DB 1583 CTTCTCCAGCTCTACCTTTACTC 1606

RESULT 12

ABL40754

ID ABL40754 standard; cDNA; 2095 BP.

XX AC

XX ABL40754;

XX XX

XX 03-JUL-2002 (first entry)

XX DE

XX Human TLCC-2 protein encoding cDNA.

XX OS

XX Homo sapiens.

XX KW

XX Transient receptor potential like calcium channel; TRP; TLCC-2; human;

XX neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;

XX cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy;

XX calcium signaling; gene; ss.

XX XX

XX Homo sapiens.

XX OS

XX Homo sapiens.

XX FT

XX Key Location/Qualifiers

XX CDS

XX 141..1883

XX FT

XX /tag= a

XX FT

XX /product= "TLCC-2"

XX FT

XX /note= "Transient receptor potential-like calcium

XX Channel"

XX FT

XX FT

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XX FT

CC disorders, learning or memory disorders such as amnesia, age-related
CC memory loss, or a neurological disorder such as migraine. The molecules
CC are also useful to treat a pain disorder. The present sequence represents
CC a cDNA encoding the human TLCC-2 polypeptide.

XX SQ Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;

Query Match 70.8%; Score 142.4; DB 24; Length 2095;

Best Local Similarity 99.3%; Pred. No. 1.8e-28;

Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GCAGTTCGCTCAGTTCATCGTGTCTGAGTGCCTTTCTCGCTCATCAATGGGACGA 117

Db 1496 GAAGTTCGCTCAGTTCATCGTGTCTGAGTGCCTTTCTCGCTCATCAATGGGACGA 1555

QY 118 CATGTTGTGAGCTTCGCGCCATGCGAGCGAGCGCCGAGCGCTGTGTGGCT 177

Db 1556 CATGTTGTGAGCTTCGCGCCATGCGAGCGAGCGCCGAGCGCTGTGTGGCT 1615

QY 178 CTTCTCCAGCTCTACCTTTACTC 201

Db 1616 CTTCTCCAGCTCTACCTTTACTC 1639

RESULT 13

AAI71699

ID AAI71699 standard; cDNA; 2095 BP.

XX AC AAI71699;

XX DT 29-JAN-2002 (first entry)

XX DE Human TRP-like calcium channel TLCC-2 coding sequence #1.

XX KW Human; TLCC-2; TRP-like calcium channel; membrane excitability;

XX KW nociception; nootropic; neuroprotective; antiparkinsonian; cytoskeletal;

XX KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquilizer;

XX KW Parkinson's disease; Huntington's disease; multiple sclerosis;

XX KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;

XX KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder; ss.

XX OS Homo sapiens.

XX FN WO200177331-A1.

XX PD 18-OCT-2001.

XX FH Key Location/Qualifiers

XX FT 141..1883

XX FT /*tag= a

XX FT /product= "TLCC-2"

XX PN WO200177331-A1.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-US11442.

XX PR 07-APR-2000; 2000US-0544797.

XX PA (MILL-) MILLENIUM PHARM INC.

XX PI Curtis RAJ, Silos-Santiago I;

XX PS WPI; 2002-010913/01.

XX DR P-PSDB; AAM51858.

XX XX

XX PT Novel isolated human transient receptor potential-like calcium channel

XX PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,

XX PT pain disorder, and cancer -

XX PS Claim 1; Fig 1; 148pp; English.

XX XX

XX CC The present invention relates to the protein and coding sequences of

XX CC human transient receptor potential (TRP)-like calcium channel protein-2

XX CC (TLCC-2). The sequences can be used in the treatment of TLCC-2 related

XX CC disorders, including central nervous system disorders such as

CC Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis,
CC Gilles de la Tourette's syndrome, autonomic function disorders, learning
CC or memory disorders, pain disorders and disorders of cellular
CC proliferation, including cancer. The present sequence is the TLCC-2
CC coding sequence including the 3' UTR.

XX SQ Sequence 2095 BP; 388 A; 682 C; 594 G; 431 T; 0 other;

Query Match 70.8%; Score 142.4; DB 24; Length 2095;

Best Local Similarity 99.3%; Pred. No. 1.8e-28;

Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GCAGTTCGCTCAGTTCATCGTGTCTGAGTGCCTTTCTCGCTCATCAATGGGACGA 117

Db 1496 GAAGTTCGCTCAGTTCATCGTGTCTGAGTGCCTTTCTCGCTCATCAATGGGACGA 1555

QY 118 CATGTTGTGAGCTTCGCGCCATGCGAGCGAGCGCCGAGCGCTGTGTGGCT 177

Db 1556 CATGTTGTGAGCTTCGCGCCATGCGAGCGAGCGCCGAGCGCTGTGTGGCT 1615

QY 178 CTTCTCCAGCTCTACCTTTACTC 201

Db 1616 CTTCTCCAGCTCTACCTTTACTC 1639

RESULT 14

AAS89318/c

ID AAS89318 standard; cDNA; 635 BP.

XX AC AAS89318;

XX DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #25122.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX KW Homo sapiens.

XX OS Homo sapiens.

XX FN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Dmanac RT, Liu C, Tang YT;

XX XX

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABG25131.

XX XX

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity -

XX PS Claim 1; SEQ ID No 25122; 103pp; English.

XX XX

XX CC The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX CC and gene mapping, and in recombinant production of (II). The

XX CC polynucleotides are also used in diagnostics as expressed sequence tags

XX CC for identifying expressed genes. (I) is useful in gene therapy techniques

XX CC to restore normal activity of (II) or to treat disease states involving

XX CC (II). (II) is useful for generating antibodies against it, detecting or

XX CC quantitating a polypeptide in tissue, as molecular weight markers and as

XX CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 635 BP; 147 A; 171 C; 210 G; 107 T; 0 other;

Query Match 70.0%; Score 140.8; DB 23; Length 635;
Best Local Similarity 98.6%; Pred. No. 3.8e-28;
Matches 142; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GCAGTTTCGGCTCACTCTCCATGGTGTCTGAGTGGCTGTTCGGTCAATCGGGACGA 117
Db 321 GAAGTTCGGCTCACTCTCCATGGTGTCTGAGTGGCTGTTCGGTCAATCGGGACGA 262

QY 118 CATGTTTGTGACGGTTCGGCCGATCGACGGCGCAGACGGCCGACGCTGTGTGGCT 177
Db 261 CATGTTTGTGACGGTTCGGCCGATCGACGGCGCAGACGGCCGACGCTGTGTGGCT 202

QY 178 CTTCCTCCAGCTCTACCTTTTACTC 201
Db 201 CTTCCTCCAGCTCTACCTTTTACTC 178

RESULT 15
AAI61022/c
ID AAI61022 standard; cDNA; 1619 BP.
XX
AC AAI61022;
XX
XX 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 5011.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukemia; ss.
XX
OS Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 03-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue A, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
DR P-PSDB; AAM41866.

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%

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25: /SIDSI/gcgdata/genseq/genseqn-emb1/NA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1489	99.2	20046	22	AAK73826 Human immune/haema
2	1463.4	97.5	11365	22	AAK73827 Human immune/haema
3	232.8	15.5	776	23	AAK65931 DNA encoding novel
4	210	14.0	33147	22	AAK67282 Human immune/haema
5	209	13.9	47999	25	AAK52898 Human tweety homol
6	208.4	13.9	711	22	AAK82492 Human immune/haema
7	208.4	13.9	50000	24	ABA98944 Human asthma-assoc
8	208.2	13.9	15765	22	ABA17911 Human nervous syst

C	9	208.2	13.9	15765	22	ABA18250	Human nervous syst
C	10	208.2	13.9	15765	22	ABA18276	Human nervous syst
C	11	208.2	13.9	15765	22	ABA19009	Human nervous syst
C	12	208.2	13.9	21444	22	AAK89645	Human digestive sy
C	13	207.8	13.8	9359	22	AAK73225	Human immune/haema
C	14	207.6	13.8	566	23	ABV44771	Human prostate exp
C	15	207.4	13.8	54877	22	AAK86026	Human immune/haema
C	16	207.4	13.8	54877	25	ABZ74225	Secreted protein g
C	17	207.4	13.8	54877	25	ABZ67791	Human secreted pro
C	18	207	13.8	14769	22	AAK04404	Human reproductive
C	19	206.8	13.8	711	22	AAK82495	Human immune/haema
C	20	206.6	13.8	122748	24	ABT10719	Human breast cance
C	21	206.2	13.7	139389	24	ABK84795	Human CDNA differe
C	22	206	13.7	21470	23	ABK42270	Genomic sequence #
C	23	205.8	13.7	19199	22	AAK70995	Human immune/haema
C	24	205.8	13.7	20188	22	AAK73082	Human immune/haema
C	25	205.8	13.7	20188	22	AAK87550	Human immune/haema
C	26	205.8	13.7	32204	22	AAK39620	Genomic sequence #
C	27	205.8	13.7	32204	22	AAK89019	Human digestive sy
C	28	205.8	13.7	32204	22	AAK91533	Human digestive sy
C	29	205.8	13.7	32204	22	AAI57790	Human colorectal c
C	30	205.8	13.7	32204	24	ABS99967	Genomic DNA #171 e
C	31	204.8	13.6	31584	22	AAK81054	Human immune/haema
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C	33	204.6	13.6	1746	22	AAI62586	Human breast or ov
C	34	204.6	13.6	1746	22	AAI03369	Human reproductive
C	35	204.6	13.6	1746	22	AAI62587	Human breast or ov
C	36	204.6	13.6	160771	24	ABQ88179	Human osteoblast d
C	37	204.6	13.6	222930	24	ABK84349	Human CDNA differe
C	38	204.4	13.6	486	23	ABV38984	Human prostate exp
C	39	204.4	13.6	154465	24	AAK28763	Human AKAP allelic
C	40	204.4	13.6	158245	24	AAK28762	Human AKAP allelic
C	41	204.4	13.6	161425	22	AAH02340	Human AKAP10 gene
C	42	204.4	13.6	162025	22	AAH02339	Human AKAP10 gene
C	43	204.4	13.6	162025	24	ABD28758	Human AKAP allelic
C	44	204.4	13.6	162025	24	ABD28759	Human AKAP allelic
C	45	204.2	13.6	5881	22	AAK07230	Human reproductive

ALIGNMENTS

RESULT 1
AAK73826
ID AAK73826 standard; DNA; 20046 BP.

XX AC AAK73826;

XX DT 07-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28638.

XX DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX KW Cytostatic; gene therapy; vaccine; metastasis; ds.

XX OS Homo sapiens.

XX PN WO200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01354.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent
 CC disease and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 20046 BP; 4133 A; 5821 C; 5659 G; 4433 T; 0 other;

Query Match 99.2%; Score 1489; DB 22; Length 20046;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1500; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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 DB 4162 CTGGGCGCGTATCGGTATGTCGCTGGTGGGGTGACCTTGACCAATGGCTCAGGGCTT 4220
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 QY 361 GCCACGTAGGAAGACCTTGTCTCTACGCACACAAATTTAGCTGGGCGTGGTGGCGTGC 420
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 QY 781 ACTCCCTGTCTTAGACTGATCCAGTGTGATCCCGGCGCCCTGAGGCCCTTCCCGGCG 840
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QY 841 GCGAGATCTACCTCTCTGGAAGCAGCTCAGTTACAGAACCTCAGCTCAATATCC 900
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RESULT 2

AAK73827

ID AAK73827 standard; DNA; 11365 BP.

XX AAK73827;

XX AAK73827;

XX 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28639.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cytosolic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

XX WO2001:57182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

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PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
metastasis -

PS Disclosure; SEQ ID NO 28639; 3071pp + Sequence Listing; English.

XX

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAK82169 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 11365 BP; 2407 A; 3320 C; 3153 G; 2485 T; 0 other;

Query Match 97.5%; Score 1463.4; DB 22; Length 11365;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1497; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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QY 61 CTGGCGCGGTATGCGTATGTCGCGTGGTGGGCTGACCTTGGACCAATGGCTCAGGGCTT 120
DB 4162 CTGGCGCGGTATGCGTATGTCGCGTGGTGGGCTGACCTTGGACCAATGGCTCAGGGCTT 4221

QY 121 GCTCTCTCCAGCGGTACTACACCGAGGCGACGTGGACCGCGGCAACGACACATTTGAC 180
DB 4222 GCTCTCTCCAGCGGTACTACACCGAGGCGACGTGGACCGCGGCAACGACACATTTGAC 4281

QY 181 ATTGATCCGATGGTGTACTGTCAGTGGGCGGACGAGCGTTCACCTGTTGGGAGCGTG 240
DB 4282 ATTGATCCGATGGTGTACTGTCAGTGGGCGGACGAGCGTTCACCTGTTGGGAGCGTG 4341

QY 241 AGCTGCTGGGATTAATCAACAGCTGTGGTGGGCGACGGTGGCTCAAGCTTAATATACC 300
DB 4342 AGCTGCTGGGATTAATCAACAGCTGTGGTGGGCGACGGTGGCTCAAGCTTAATATACC 4401

QY 301 AGCACTTTGGAGGCTGAGGAGGAGGATTCGTTGAGGCGCGAAGTTTGGACACGACGCTG 360
DB 4402 AGCACTTTGGAGGCTGAGGAGGAGGATTCGTTGAGGCGCGAAGTTTGGACACGACGCTG 4461

QY 361 GGCCACGTAGGAAGACCTTGCTCTACGCAACAACAATAGCTGGGCGTGTGCGGTGC 420
DB 4462 GGCCACGTAGGAAGACCTTGCTCTACGCAACAACAATAGCTGGGCGTGTGCGGTGC 4521

QY 421 CCCTGTGCTCCAGCTACTCAGGAGGCTGAGGCGAGGAGATCGCTTGAGTCCGGAGGTT 480
DB 4522 CCCTGTGCTCCAGCTACTCAGGAGGCTGAGGCGAGGAGATCGCTTGAGTCCGGAGGTT 4581

QY 481 GAGGCTGAGTAAAGCTATGACACGCTGCTGCACTCCACCTTGGGTGACAGAGTGAACC 540
DB 4582 GAGGCTGAGTAAAGCTATGACACGCTGCTGCACTCCACCTTGGGTGACAGAGTGAACC 4641

QY 541 CTGTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 600
DB 4642 CTGTCTC-AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 4700

QY 601 GCCACGTAGAAAGCACCAAGATGTTATATTTAATATGCTCATTGAGTAAATCAATCCGCA 660
DB 4701 GCCACGTAGAAAGCACCAAGATGTTATATTTAATATGCTCATTGAGTAAATCAATCCGCA 4760

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DB 4761 GGCCACGAGAGTCCAGCGCTGTAGGAATGACCAACCTTGGGAGACACAGGGAAGAAG 4820

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DB 4821 GCCACTGGGGACTCTGGGGAGACCAAGCTGCGCTCCCGGCGCCCTTCCCTGAGGCGCTTCCCTG 4880

QY 781 ACTCCCTGTCTTCCCTAGACCTGATCCAGGTGGATCCCGGAGCGGCGCCCTTCCCGCCCCCA 840

DB 4881 ACTCCCTGTCTTCCCTAGACCTGATCCAGGTGGATCCCGGAGCGGCGCCCTTCCCGCCCCCA 4940

QY 841 CGGACGATCTCACCTCTTGGAAAGCAGCTCCAGTTACAAGAACTCAAGCTCAAAATTC 900

DB 4941 CGGACGATCTCACCTCTTGGAAAGCAGCTCCAGTTACAAGAACTCAAGCTCAAAATTC 5000

QY 901 ACAAGTACTGCTCTCACTCAGGCGGCGCCAGGCTGGGGAGGAGCAGACACTAGGCAC 960

DB 5001 ACAAGTACTGCTCTCACTCAGGCGGCGCCAGGCTGGGGAGGAGCAGACACTAGGCAC 5060

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DB 5120 CTGCTGGGTGAGCACTTCCCTGCGAGTGCAGAGTCAGCACGTGGCAGGGAGCGCTGCG 5179

QY 1081 ACTTTGGGCGGAGGAGCGGAGCGCCCTGACCTCACTCCGAGCGCTTCTGCTGCTAGG 1140

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QY 1141 CTGCTCAATGTCACTATCCACTTCCGGCTGAAGACCACTTAACCTCCAGAGCGCTCATCAAT 1200

DB 5240 CTGCTCAATGTCACTATCCACTTCCGGCTGAAGACCACTTAACCTCCAGAGCGCTCATCAAT 5299

QY 1201 AATGAGATCCCGGACTGCTATACCTTCAGGCTCTGCTGAGCGCCCGCGGAAACCCACAG 1260

DB 5300 AATGAGATCCCGGACTGCTATACCTTCAGGCTCTGCTGAGCGCCCGCGGAAACCCACAG 5359

QY 1261 GGCTCTCAGTTCCAGGCGGAGCGCTGTCAGGAGTGTCTTGGGAGCACTGGCCAGG 1320

DB 5360 GGCTCTCAGTTCCAGGCGGAGCGCTGTCAGGAGTGTCTTGGGAGCACTGGCCAGG-G 5418

QY 1321 GCAAGCGTGGGGGTGATGAGGGAGGAGCGCGGGTCTGTGAGGCCACCTGTCTATGTGA 1380

DB 5419 GCAAGCGTGGGGGTGATGAGGGAGGAGCGCGGGTCTGTGAGGCCACCTGTCTATGTGA 5478

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DB 5479 CTTGGGGCTTGGGGCTGCGCAAGTTTACTCTGCCCCCAACTGGCCCCCAGATCACGT 5538

QY 1441 TTGACAAACAAGCACACAGTGGCGGATCCCAATCAGCTGGAGACCCAGGCCACATCC 1500

DB 5539 TTGACAAACAAGCACACAGTGGCGGATCCCAATCAGCTGGAGACCCAGGCCACATCC 5598

QY 1501 A 1501

DB 5599 A 5599

RESULT 3
AAK54951
ID AAK565931 standard; cDNA; 776 BP.

XX AAK565931;
AC AAK565931;
XX
DT 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #1735.
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS
XX
EN W0200175067-A2.
XX

PD 11-OCT-2001.
 XX AC
 XX 30-MAR-2001; 2001WO-US08631.
 XX DT
 XX 31-MAR-2000; 2000US-0540217.
 PR PR
 PR 23-AUG-2000; 2000US-0649167.
 XX XX
 PA (HYSE-) HYSEQ INC.
 XX XX
 XX Drmanac RT, Liu C, Tang YT;
 PI PI
 XX WPI; 2001-639362/73.
 XX DR
 DR P-PSDB; ABG01744.
 XX XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX XX
 PS Claim 1; SEQ ID NO 1735; 103pp; English.
 XX XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (I) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX XX
 SQ Sequence 776 BP; 141 A; 243 C; 248 G; 144 T; 0 other;
 Query Match 15.5%; Score 232.8; DB 23; Length 776;
 Best Local Similarity 98.8%; Pred. No. 1.5e-46;
 Matches 245; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 34 CAGTACTGGCGTTCCTGACGTGCTCACTGGGCGGCTATCGGTGCTGGGGGT 93
 Db 529 CAGTACTGGCGTTCCTGACGTGCTCACTGGGCGGCTATCGGTGCTGGGGGT 588
 QY 94 GACCCTTGGACCAATGCTCAGGGTGTCTCTGCGACGGGTACTACACCGAGGCCAC 153
 Db 589 GACCCTTGGACCAATGCTCAGGGTGTCTCTGCGACGGGTACTACACCGAGGCCAC 648
 QY 154 GTGACCCGCGCCACGACACATTTCATTCAT-CCGATGGTGGTACTGGTGGGCG 212
 Db 649 GTGACCCGCGCCACGACACATTTCATTCATTCGCGATGGTGGTGGGCG 708
 QY 213 AGGACGAGGCTTCACTCTGGGAGCCTGAGCTGCTGGGATTAATAATCAACAGCTGTGGCT 272
 Db 709 AGGACGAGGCTTCACTCTGGGAGCCTGAGCTGCTGGGATTAATAATCAACAGCTGTGGCT 768
 QY 273 GGGCACGG 280
 Db 769 GGGCACGG 776
 RESULT 4
 AAK67282
 ID AAK67282 standard; DNA; 33147 BP.

XX AC
 XX 06-NOV-2001 (first entry)
 XX DT
 XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094.
 DE DE
 XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 KW Homo sapiens.
 OS OS
 XX WO200157182-A2.
 XX PN
 XX 09-AUG-2001.
 PD PD
 XX 17-JAN-2001; 2001WO-US01354.
 PF PF
 XX 31-JAN-2000; 2000US-0179065.
 PR PR
 PR 04-FEB-2000; 2000US-0180628.
 PR PR
 PR 24-FEB-2000; 2000US-0184664.
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 PR 02-MAR-2000; 2000US-0186350.
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 PR 18-APR-2000; 2000US-0198123.
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 PR 19-MAY-2000; 2000US-0205515.
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 PR 07-JUL-2000; 2000US-0216847.
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 PR 11-JUL-2000; 2000US-0217487.
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 PR 11-JUL-2000; 2000US-0217496.
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 PR 14-JUL-2000; 2000US-0218290.
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 PR 26-JUL-2000; 2000US-0220963.
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 PR 26-JUL-2000; 2000US-0220964.
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 PR 14-AUG-2000; 2000US-0224518.
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 PR 14-AUG-2000; 2000US-0224519.
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 PR 14-AUG-2000; 2000US-0225214.
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 PR 14-AUG-2000; 2000US-0225266.
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 PR 14-AUG-2000; 2000US-0225270.
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 PR 14-AUG-2000; 2000US-0225270.
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 PR 14-AUG-2000; 2000US-0225447.
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 PR 14-AUG-2000; 2000US-0225757.
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 PR 14-AUG-2000; 2000US-0225758.
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 PR 14-AUG-2000; 2000US-0225759.
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 PR 18-AUG-2000; 2000US-0226279.
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 PR 22-AUG-2000; 2000US-0226681.
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 PR 22-AUG-2000; 2000US-0227182.
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 PR 23-AUG-2000; 2000US-0227009.
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 PR 30-AUG-2000; 2000US-0228924.
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 PR 01-SEP-2000; 2000US-0229287.
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 PR 05-SEP-2000; 2000US-0229509.
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 PR 05-SEP-2000; 2000US-0229513.
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 PR 06-SEP-2000; 2000US-0230437.
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 PR 06-SEP-2000; 2000US-0230438.
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 PR 08-SEP-2000; 2000US-0231242.
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 PR 08-SEP-2000; 2000US-0231243.
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 PR 08-SEP-2000; 2000US-0231244.
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 PR 08-SEP-2000; 2000US-0231413.
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 PR 08-SEP-2000; 2000US-0231414.
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 PR 08-SEP-2000; 2000US-0232080.
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 PR 08-SEP-2000; 2000US-0232081.
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 PR 12-SEP-2000; 2000US-0231968.
 PR PR
 PR 14-SEP-2000; 2000US-0232397.
 PR PR
 PR 14-SEP-2000; 2000US-0232398.
 PR PR
 PR 14-SEP-2000; 2000US-0232399.

RESULT 6
AAK82492
ID AAK82492 standard; DNA; 711 BP.
XX AC AAK82492;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37304.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX OS Homo sapiens.
XX FN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 11-JUL-2000; 2000US-0217487.
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PR 26-JUL-2000; 2000US-0220964.
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PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
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PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.

PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 37304; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 711 BP; 232 A; 131 C; 167 G; 181 T; 0 other;
SQ
Query Match 13.9%; Score 208.4; DB 22; Length 711;
Best Local Similarity 81.2%; Pred. No. 1.2e-40;
Matches 255; Conservative 0; Mismatches 56; Indels 3; Gaps 1;
QY 269 GGCTGGGCGGAGTGGCTGAGTATATACAGCAGCTTTGGAGGCTGAGGAGGAAGGA 328
Db 117 GGCGGGGCGAGTGGCTGAGTATATACAGCAGCTTTGGAGGCGGAGTGGGCGAG 176
QY 329 TTGCTTGAGGCCAGAGTATTTAGACACAGCTGGGCGACGTAGGAGACCTTGTCTTAC- 387
Db 177 TCACCTGAGGTGAGAGTTTGGAGCAGCAGCTGGGCAACATGACAAACCCGCTCTACT 236
QY 388 --GCACAAACAAATTTAGTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 445
Db 237 AAAGATACAAATTTATCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 296
QY 446 GCTGAGGCGAGGAGTATCTGAGTCCGCGAGGTTGAGGCTGGAGTGAAGTATGACACAG 505
Db 297 GCTGAGGCGAGGAGTATCTGTTGACCCAGGAGTGGAGGTTGAGTGAAGTATGACACAG 356
QY 506 CTGCTGACCTCCAGCTGGGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 565
Db 357 CCACTGACCTCCAGCTGGGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 416
QY 566 AAAAAACAAAGTATG 579
Db 417 AAAAAACAAAGTATG 430

RESULT 7

ABA98944
ID ABA98944 standard; DNA; 50000 BP.
XX
XX ABA98944;
AC
XX
DT 18-JUN-2002 (first entry)
XX
DE Human asthma-associated gene AAGB genomic DNA #1.
XX
KW Human; asthma; AAGB; antiinflammatory; antiasthmatic; ARDS; COPD; COAD;
KW inflammatory disease; obstructive airways disease; dyspnea; emphysema;
KW adult respiratory distress syndrome; chronic bronchitis; eosinophil;
KW chronic obstructive pulmonary disease; pneumoconiosis;
KW chronic obstructive airways disease; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200206312-A2.
XX
XX 24-JAN-2002.
PD
XX
PP 11-JUL-2001; 2001WO-EP08010.
XX
PP 13-JUL-2000; 2000US-0615247.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Whittaker PA;
XX
XX WPI; 2002-195799/25.
DR
XX Novel polypeptide encoded by disease associated gene, useful for
PT treating an inflammatory or obstructive airways disease e.g. asthma -
PT
XX
PS Claim 3; Page 44-57; 70pp; English.
XX
CC The sequence represents a human asthma associated gene (AAGB) genomic DNA
CC sequence. The invention relates to a novel asthma-associated gene AAGB
CC and the polypeptide encoded by AAGB. The polypeptide of the invention has
CC antiinflammatory and antiasthmatic activity, and may have a use in gene
CC therapy, or as a vaccine. The polypeptide, polynucleotide, antibody and
CC antisense oligonucleotide of the invention (collectively referred to as
CC agents) are useful for treating an inflammatory or obstructive airways
CC disease. They are also useful for are useful for treating adult
CC respiratory distress syndrome (ARDS), chronic obstructive pulmonary or
CC airways disease (COPD or COAD), including chronic bronchitis or dyspnea
CC associated with it, emphysema, exacerbation of airways hyper-reactivity
CC consequent to other drug therapy and pneumoconiosis. The agents are also
CC useful in the treatment of eosinophil related disorders and asthma.
XX
SQ Sequence 50000 BP; 14069 A; 9489 C; 10164 G; 16278 T; 0 other;
Query Match 13.9%; Score 208.4; DB 24; Length 50000;
Best Local Similarity 81.2%; Pred. No. 5 se-40;
Matches 255; Conservative 0; Mismatches 56; Indels 3; Gaps 1;
QY 269 GGCTGGGCGGAGTGGCTGAGTATATACAGCAGCTTTGGAGGCTGAGGAGGAAGGA 328
Db 40714 GGCGGGGCGAGTGGCTGAGTATATACAGCAGCTTTGGAGGCGGAGTGGGCGAG 40773
QY 329 TTGCTTGAGGCCAGAGTATTTAGACACAGCTGGGCGACGTAGGAGACCTTGTCTTAC- 387
Db 40774 TCACCTGAGGTGAGAGTTTGGAGCAGCAGCTGGGCAACATGACAAACCCGCTCTACT 40833
QY 388 --GCACAAACAAATTTAGTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 445
Db 40834 AAAGATACAAATTTATCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 40893
QY 446 GCTGAGGCGAGGAGTATCTGAGTCCGCGAGGTTGAGGCTGGAGTGAAGTATGACACAG 505

Db 40894 GCTGAGCGCAAGAAATGCTTGAACCCAGGAGGTGGAGTTCGAGTGGCAAGATCACA 40953
QY 506 CTGCTGCACTCCACCTCGGTGACAGAGTGAGACCCCTGCTCAAAAAA 565
Db 40954 CCACTGCACTCCAGCTGGCGCAGAGCGAGACTCTGCTCAAAAAA 41013
QY 566 AAAAAACAAGTATG 579
Db 41014 AAAAAAAGATG 41027

RESULT 8
ABAl7911/c
ID ABAl7911 standard; DNA; 15765 BP.
XX ABAl7911;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 10242.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; viruicide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
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PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
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PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
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PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
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 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

PI WPI; 2001-541565/60.

DR Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 FT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 PT
 XX
 XX Disclosure; SEQ ID NO 10242; 1701pp + Sequence Listing; English.

XX The invention relates to novel genes (ABA1004-ABA21534) and proteins

CC (AB314678-AB318001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases such as cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 15765 BP; 4553 A; 3137 C; 3376 G; 4699 T; 0 other;

Query Match 13.9%; Score 208.2; DB 22; Length 15765;
 Best Local Similarity 79.5%; Pred. No. 4e-40;
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QY 312 AGGCTGAGGAGGAGGATTTGTTGAGGCGCAGCAAGTTTGAGACCAAGCTGGGCGCACGTAGG 371

DB 4124 AGGCTGAGGTTGGCGGATCACTGTAGGTTGAGAGTTTGAGACCAAGCTGGCGCACATGGC 4065

QY 372 AAGACCTTGTCTTACGCACAA-----ACAAATTAGCTGGCGCTGGTGGCTGCCCTGTG 427
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 QY 548 AAAAAAAAAAAAAAAAAAAAAA 574
 DB 3884 AAAAAAAAAAAAAAAAAAAAAA 3858

RESULT 9

ABA18250/c

ID ABA18250 standard; DNA; 15765 BP.

XX AC ABA18250;

XX DT 23-JAN-2002 (first entry)

XX DE Human nervous system related polynucleotide SEQ ID NO 10581.

XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;

XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

XX KW antiparkinsonian; antisickling; antianemic; antiarthritic; cancer;

XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;

XX KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;

XX KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;

XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX OS Homo sapiens.

XX PN WO200159063-A2.

XX PD 16-AUG-2001.

XX 17-JAN-2001; 2001WO-US01334.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184624.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

XX 26-JUL-2000; 2000US-0220964.

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XX 14-AUG-2000; 2000US-0225268.

XX 14-AUG-2000; 2000US-0225270.

XX 14-AUG-2000; 2000US-0225447.

XX 14-AUG-2000; 2000US-0225757.

XX 14-AUG-2000; 2000US-0225758.

XX 14-AUG-2000; 2000US-0225759.

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PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 10581; 1701pp + Sequence Listing; English.

The invention relates to novel genes (AB11004-AB21534) and proteins (AB114678-AB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp:wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 15765 BP; 4553 A; 3137 C; 3376 G; 4699 T; 0 other;

Query Match

Best Local Similarity 13.9%; Score 208.2; DB 22; Length 15765;

Matches 260; Conservative 0; Mismatches 63; Indels 4; Gaps 1;

QY

252 TTAATAATCAACAGCTGTGGCTGGCGACGGTGTACGCTATATACCACTTTGGG 311

Db 4184 TGAAGTTTATGTAATGCGCGGCGACGGTGGCTCACACCTATAATCCAGCATTGGG 4125
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Qy 428 GTCCAGCTACTCAGGAGGTGAGGAGGAGGATCGCTTGAAGTCCGGAGGTTGAGGCTG 487
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Qy 548 AAAAAAAAAAAAAAAAAAAAAA 574
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ID AB18276 standard; DNA; 15765 BP.

XX AC AB18276;

XX AC AB18276;

XX DT 23-JAN-2002 (first entry)

XX DE Human nervous system related polynucleotide SEQ ID NO 10607.

XX KW Human; neotropic; neuroprotective; cytostatic; dermatological; viricide;

XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;

XX KW antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;

XX KW antirheumatic; hepatotropic; cerebrotective; antinflammatory;

XX KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;

XX KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;

XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX OS Homo sapiens.

XX OS WO200159063-A2.

XX PN 16-AUG-2001.

XX PD 17-JAN-2001; 2001WO-US01334.

XX PF 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

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PR 29-SEP-2000; 2000US-0236368.
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PR 29-SEP-2000; 2000US-0236370.
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 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-541565/60.
 Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 useful for preventing, diagnosing and/or treating nervous system
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 Disclosure; SEQ ID NO 10607; 1701pp + Sequence Listing; English.
 The invention relates to novel genes (ABA1004-ABA21534) and proteins
 (AB114678-AB18001) useful for preventing, treating or ameliorating
 medical conditions e.g. by protein or gene therapy. The genes are
 isolated from a range of human tissues disclosed in the specification.
 The nucleic acids, proteins, antibodies and (ant)agonists are useful
 in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 and ovarian cancer and other cancers of the adrenal gland, bone, bone
 marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 and parasitic infections.
 Note: The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Sequence 15765 BP; 4553 A; 3137 C; 3376 G; 4699 T; 0 other;

Query Match 13.9%; Score 208.2; DB 22; Length 15765;
 Best Local Similarity 79.5%; Pred. No. 4e-40;
 Matches 260; Conservative 0; Mismatches 63; Indels 4; Gaps 1;
 QY 252 TTAATCAACAGCTGTGGTGGGCACGGTGGCTCAGCCTATATAATCAACACTTTGGG 311
 DB 4184 TGAAGTTTATGTAATGGCGGCGACGGTGGCTCACACTATAATCCAGCACTTTGGG 4125
 QY 312 AGCTGAGGAGGAAGGATTCCTTGAGGCCAGAGTTTGGAGCCAGCCTGGGCCACGTAGG 371
 DB 4124 AGGCTGAGGTGGCGGATCACCTGAGGTGAGGATTTGAGACCAAGCTGGCCACATGGC 4065
 QY 372 AAGACCTTGTCTCTACACCAA-----ACAAATTAGCTGGGCGTGGTGGCGCCCTGTG 427
 DB 4064 AAAACCTGTCTCTACTTAAAGTGCAAAATTAACCGGATATGTTGGTGACACCTGTA 4005
 QY 428 GTCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGTTGAGTCCGGAGTTGAGGCTG 487
 DB 4004 ATCCAGCTACTCAGGAGGCTGAGGCAGGAGGATCGTTGAAACCCAGGAGTGAAGTTG 3945
 QY 488 CAGTAAGCTATGACCACGCTGCTGCACCTCCACCTGCGTGACAGTGAACCTGTCTC 547
 DB 3944 CAGTGAAGTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3885
 QY 548 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 574
 DB 3884 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3858
 RESULT 11
 ABA19009/C
 ID ABA19009 standard; DNA; 15765 BP.
 XX AC ABA19009;
 XX XX
 DT 23-JAN-2002 (first entry)
 XX DE Human nervous system related polynucleotide SEQ ID NO 11340.
 XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antineoplastic; anti-infectious; anti-HIV; antibacterial; vulnary;
 KW antiparkinsonian; antisickling; antianemic; antidiabetic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX OS Homo sapiens.
 XX PN WO200159063-A2.
 XX PD 16-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US01334.
 XX PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209457.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.

CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX
SQ Sequence 15765 BP; 4553 A; 3137 C; 3376 G; 4699 T; 0 other;
Query Match 13.9%; Score 208.2; DB 22; Length 15765;
Best Local Similarity 79.5%; Pred. No. 4e-40;
Matches 260; Conservative 0; Mismatches 63; Indels 4; Gaps 1;
Qy 252 TTAATAACAACAGCTGTGGCTGGGACGCTGGCTCACGCCCTATAATACAGCACTTTGGG 311
Db 4184 TGAAGTTTATGTAATGCGCGGCAACGCTGCTCACACCTATAATCCAGCACTTTGGG 4125
Qy 312 AGGCTGAGGAGAGGATTGCTTGAGGCCAGAAAGTTTGAGCCAGCCCTGGGCCACGTAGG 371
Db 4124 AGGCTGAGTGGGCGGATCAGCTGAGTTCAGAGCTTTCAGACCACTGGCCCAACATGGC 4065
Qy 372 AAGACCTTGTCTCTACGCACAA---ACAATTAGCTGGCGTGGTGGCGCCCTGTG 427
Db 4064 AAAACCTTGTCTCTACTAAAGTGCAAAATTAGCCGATATGTTGGTGCACACCTGTA 4005
Qy 428 GTCCAGCTACTCAGAGGCTGAGGAGGATCGCTTGAGTCCGGAGGTTGAGGCTG 487
Db 4004 ATCCAGCTACTCAGAGGCTGAGGAGGATCGCTTGAGTCCGGAGGTTGAGGCTG 3945
Qy 488 CAGTAAGCTATGACCAAGCTGCTGCTCCACCTGGTGGTGCAGAGTGAGACCCCTGTCTC 547
Db 3944 CAGTGAGTCGAGATCATGCCACTCCAGCTGGTGGTGCAGAGCAAGACCTTGTCTC 3885
Qy 548 AAAAAAAAAAAAAAAAAAAAAAA 574
Db 3884 AAAAAAAAAAAAAAAAAAAAAAA 3858

RESULT 12

AAK89645/c

ID AAK89645 standard; DNA; 21444 BP.

XX AC AAK89645;
XX

DT 05-NOV-2001 (first entry)

XX DE Human digestive system antigen genomic sequence SEQ ID NO: 3221.

XX KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.

XX OS Homo sapiens.

XX PN WO200155314-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01324.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214885.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 07-JUL-2000; 2000US-0216880.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 11-JUL-2000; 2000US-0217496.

XX PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
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PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236327.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.

PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
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 PR 08-NOV-2000; 2000US-0246526.
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 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
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 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-502630/55.
 DR
 XX
 PT Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases -
 XX
 XX Disclosure; SEQ ID NO 3221; 986pp; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human digestive system antigens. These can be used in the
 CC diagnosis, treatment and prevention of digestive system disorders,
 CC including cancer, Meckel's diverticulum, bacterial or parasitic
 CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
 CC ulcerative colitis. The present sequence is a genomic DNA fragment
 CC encoding a digestive system antigen of the invention.
 XX
 SQ Sequence 21444 BP; 6416 A; 4554 C; 4517 G; 5957 T; 0 other;
 Query Match 13.9%; Score 208.2; DB 22; Length 21444;
 Best Local Similarity 78.5%; Pred No. 4.5e-40;
 Matches 249; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 269 GGCTGGCCACGGTGGCTCAGCCTATAATACAGCACTTTGGAGGCTCAGGAGGAGGA 328
 |||||
 DB 17837 GGCTGGCCACAGTGGCTCTCGCATATAATCCAGCATCTTGGAGGCCGAGCAAGGA 17778
 |||||
 QY 329 TTGCTTGGAGCCAGAAAGTTTGAGACAGCCTGGGCCACCTAGGAACCTTGTCTTACG 388
 |||||
 DB 17777 TCACCTTGGAGCCAGGAGTTTCAAGACTAGCCTAGGCAATATAGGAAGACCTGCTCTAAA 17718
 |||||
 QY 389 CACAAACAAATTAGCTGGCGTGGCTGGTCCCTGTGGTCCAGCTACTCAGGAGGCT 448
 |||||
 DB 17717 AATTTAAATTAAGCCAGGTATGGTGGCTGTACCTGTAGTCCAGCTACTCAGGAGGCT 17658
 |||||
 QY 449 GAGCAGGAGGATCGTTGAGTCCGGAGGTTGAGCTGCGAGTAACTATGACACCGCTG 508
 |||||
 DB 17657 GAGTAGGAGGATCACTTGAGCCAGGAATTTGAGGCTGTAGTGAGCTATGATTGTACCA 17598
 |||||
 QY 509 CTGCACTCCACCTGGGTGACAGAGTGAGACCTGTCTCAAAAAAAAAAAAAAAAAA 568
 |||||
 DB 17597 CTGCACTCCAGCCTGGGTAAACACAGCCAGACCTGTCTCAAAAAAAAAAAAAAAAAA 17538
 |||||
 QY 569 AAACAAGTATGCTTAGT 585
 |||||
 DB 17537 AATCCATATTGTTAAT 17521
 |||||
 RESULT 13
 AAK73225
 ID AAK73225 standard; DNA; 9359 BP.
 XX
 AC AAK73225;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28037.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX
 OS Homo sapiens.
 XX
 FN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01354.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
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PR 07-JUL-2000; 2000US-0216880.
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PR 18-AUG-2000; 2000US-0226279.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
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PR 08-SEP-2000; 2000US-0232080.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
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PR 02-OCT-2000; 2000US-0236802.
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PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 08-NOV-2000; 2000US-0246476.
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PR 08-NOV-2000; 2000US-0246526.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 40838; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.

XX

SQ Sequence 54877 BP; 15008 A; 10329 C; 11472 G; 18068 T; 0 other;

Query Match 13.8%; Score 207.4; DB 22; Length 54877;

Best Local Similarity 78.2%; Pred. No. 9.9e-40;

Matches 262; Conservative 0; Mismatches 71; Indels 2; Gaps 1;

QY	254	AAATCAACAGCTGTGGCTGGGACGCTGCTCAGCGCTATATACAGCACTTTGGGAG	313
Db	32261	AAATCAAGGGGAGGCTGGGACGCTGCTCAGCGCTATATACAGCTTTGGGAG	32202
QY	314	GCTGAGGAGGAGATTGCTTTGAGGCCAGAGTTTGAGACCGCTGGGCCAGTAGGAA	373
Db	32201	GCCAGATGGGTGGAT--CATGAGGTGAGGAGTTCGAGATCAGCCTGGCCATATGCCAA	32144
QY	374	GACCTTGCTCTACGCACAAACAATAGCTGGCGGTGGCGTGCCTGTGTGCCCA	433
Db	32143	AACCCGCTCTTACTAAACAACATTTAGCAGCGGTGGCGTGCCTGTATATCCCA	32084
QY	434	GCTACTCAGGAGGCTGAGGAGGAGGATCGCTTGAAGTCGGGAGGTTGAGGCTGCAGTAA	493
Db	32083	GCTACTCGGGAAGCTGAGGAGGAGGATCGCTTGAACCCGGAGGTGGAGTTGCAGTGA	32024
QY	494	GCTATGACCGCTGTGCTGCTCCCTCCCTGGTGACAGAGTGAGACCTGTCTCAAAAA	553
Db	32023	GCCAGATTGACCACTGCACTCCAGCTGGGAGGAGGAGGAGTCTGTCTCAAAAA	31964
QY	554	AAAAAAAAAAAAAAAAAACAAGTATGCTTAGTGTG	588
Db	31963	AAAAAAAAAAAAAAAAAACAAGGGGCGCAGGTGTG	31929

Search completed: October 27, 2003, 12:34:11

Job time : 493.838 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:10:42 ; Search time 6013.64 Seconds
(without alignments)
10211.014 Million cell updates/sec

Title: US-09-851-494B-1_COPY_5500_7000

Perfect score: 1501

Sequence: 1 gccggactcacaggccctcc.....gagaccagccacatcca 1501

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_vl.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rtd.*

36: em_htg_man.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	1501	100.0	173126	9	AC008878	AF287270 Homo sapi
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4	490	32.6	579	9	AF305572S5	AC021153 Homo sapi
5	442.6	29.5	2272	9	HSA2931659	AF305572 Homo sapi
6	332	22.1	332	9	AF305572S4	AJ2931659 Homo sapi
7	227	15.1	790	9	AF305572S3	AF305575 Homo sapi
C	224.4	15.0	164293	9	AC020978	AF305574 Homo sapi
C	223.6	14.9	89666	2	AC022403	AC020978 Homo sapi
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11	223	14.9	191267	2	AC093695	AC069335 Homo sapi
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C	220	14.7	162617	9	AC007501	AC084756 Homo sapi
C	220	14.7	169202	9	AC007490	AC007501 Homo sapi
15	219.2	14.6	59634	2	AC133460	AC007490 Homo sapi
16	218.6	14.6	89653	9	AC080096	AC133460 Homo sapi
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C	218.6	14.6	170423	9	AC018663	AX647597 Sequence
C	218	14.5	151964	9	AL663038	AC018663 Human Chr
C	218	14.5	166336	9	AL445467	AL663038 Human DNA
21	217.6	14.5	83969	9	AC005210	AL445467 Human DNA
22	217.6	14.5	137718	9	AL137066	AC005210 citb.179
C	216.6	14.4	194062	9	AC138071	AL137066 Human DNA
C	215.8	14.4	184536	2	AC068682	AC138071 Homo sapi
C	215.8	14.4	218074	9	AC023283	AC068682 Homo sapi
C	215.4	14.4	95620	9	AC106753	AC023283 Homo sapi
27	214.4	14.3	188488	9	AC006057	AC106753 Homo sapi
C	214	14.3	153792	9	AC012073	AC006057 Homo sapi
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38	212.6	14.2	43987	9	AC005391	AC008130 Homo sapi
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C	212.4	14.2	160420	9	AC022023	AC108471 Homo sapi
C	212.4	14.2	171309	9	AC012146	AC022023 Homo sapi
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ALIGNMENTS

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ACCESSION AF287270
VERSION AF287270.1 GI:9844925
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 13270)
AUTHORS Sun,M., Goldin,E., Stahl,S., Falardeau,J.L., Kennedy,J.C.,
Acierio,J.S., Jr., Bove,C., Kaneski,C.R., Nagle,J., Bromley,M.C.,
Colman,M., Schiffmann,R. and Staugenhardt,S.A.

Pred. No. is the number of results predicted by chance to have a

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Mucopolidosis type IV is caused by mutations in a gene encoding a novel transient receptor potential channel
Hum. Mol. Genet. 9 (17), 2471-2478 (2000)

20485419
11030752
2 (bases 1 to 13270)
Slaugenaupt, S.A.
Direct Submission
Submitted (13-JUL-2000) Molecular Neurogenetics, Harvard Institute of Human Genetics, 77 Ave. Louis Pasteur, HIM Building Room 422, Boston, MA 02115, USA
Location/Qualifiers

FEATURES

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Best Local Similarity 100.0%; Pred. No. 0;
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Db 5620 GCTCTCTGCCAGGCTACTACACCGAGGCCACGTGGACCCCGGCCAACGACACATTGAC 5679

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Qy 241 AGCTGTGGGATTAATAATCAACAGCTGTGGCTGGGACCGTGGCTTATATATACC 300
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Qy 301 AGCATTTCGGAGGCTGAGGAGGAGGATTGCTTGAAGCCAGAGTTTGAGACCAAGCCTG 360
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Qy 361 GGCCACGTAGGAAGACCTTGTCTCTACGCACAAAACAATAGCTGGGCTGTGGCTGC 420
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Qy 481 GAGGCTGCGATAGCTATGACCAAGCTGTGCATCCACCTCTGGGTGACAGAGTGAGACC 540
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Qy 1321 GCAAGCGTGGGGTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
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ACCESSION AC008878
VERSION
KEYWORDS
SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
2 (bases 1 to 173126)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 173126)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (01-JUN-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 173126)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (12-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 12, 2002 this sequence version replaced gi:21306637.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
NOTE: This insert is not the entire sequence of the clone. It is
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Matches 1501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AC021153 155645 bp DNA linear HTG 07-JUL-2000
 Homo sapiens chromosome 19 clone RP11-492L14, WORKING DRAFT
 SEQUENCE, 20 unordered pieces.

AC021153
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Waterston, R.H.
 The sequence of Homo sapiens clone
 Unpublished
 JOURNAL
 REFERENCE
 2 (bases 1 to 155645)
 Waterston, R.H.
 Direct Submission
 Submitted (14-JAN-2000) Genome Sequencing Center, Washington
 University School of Medicine, 444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Jun 17, 2000 this sequence version replaced gi:7344405.

Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc/index.shtml>
 Project Information
 Center project name: H NH0492L14
 Summary Statistics
 Sequencing vector: M13; 82%
 Sequencing method: plasmid; 18%
 Chemistry: Dye-terminator; 77% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 141755 bases at least Q40
 Consensus quality: 145922 bases at least Q30
 Consensus quality: 148291 bases at least Q20
 Insert size: 167000; agarose-fp
 Quality coverage: 3.76 in Q20 bases; agarose-fp
 Quality coverage: 4.16 in Q20 bases; sum-of-contigs
 NOTE: This is a 'working draft' sequence. It currently
 consists of 20 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1052: contig of 1052 bp in length
 1053 1152: gap of unknown length
 1153 2714: contig of 1562 bp in length
 2715 2814: gap of unknown length
 2815 4101: contig of 1287 bp in length
 4102 4201: gap of unknown length
 4202 7146: contig of 2945 bp in length
 7147 7246: gap of unknown length
 7247 9807: contig of 2561 bp in length
 9808 12944: contig of 3037 bp in length
 12945 13044: gap of unknown length
 13045 16486: contig of 3442 bp in length
 16487 20919: contig of 4333 bp in length
 20920 26033: contig of 5014 bp in length
 26034 26133: gap of unknown length
 26134 30552: contig of 4419 bp in length
 30553 30652: gap of unknown length
 30653 35333: contig of 4681 bp in length
 35334 39655: contig of 4222 bp in length
 39656 39756: gap of unknown length
 39757 44735: contig of 4980 bp in length
 44736 44835: gap of unknown length
 44836 55751: contig of 10916 bp in length
 55752 58551: gap of unknown length
 58552 67916: contig of 12065 bp in length
 67917 77332: contig of 9316 bp in length
 77333 77432: gap of unknown length
 77433 94471: contig of 17039 bp in length
 94472 94571: gap of unknown length
 94572 113604: contig of 19033 bp in length
 113605 113705: gap of unknown length
 113706 134801: contig of 21097 bp in length
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Qy 61 CTGGCCGATATGCTATGTCGCTGGTGGGCTGACCTTGGACCAATGGCTCAGGGCTT 120
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Qy 121 GCTCTCTGCCAGCGGTACTACACAGAGCGACAGTGGACCGGCCAACAGACATTTGAC 180
Db 128281 GCTCTCTGCCAGCGGTACTACACAGAGCGACAGTGGACCGGCCAACAGACATTTGAC 128222

Qy 181 ATTGATCCGATGGTGGTACTGGTGGTGGGAGGAGGCTTCACTGTTGGGAGCCTG 240
Db 128221 ATTGATCCGATGGTGGTACTGGTGGTGGGAGGAGGCTTCACTGTTGGGAGCCTG 128162

Qy 241 AGCTGCTGGGATTAATAACAAGCTGTGGTGGGAGGAGGCTTCACTGTTGGGAGCCTG 300
Db 128161 AGCTGCTGGGATTAATAACAAGCTGTGGTGGGAGGAGGCTTCACTGTTGGGAGCCTG 128102

Qy 301 AGCACTTTGGGAGGTGAGGAGGAGGATTTGCTTGGGAGGAGGATTTGAGACAGGCTG 360
Db 128101 AGCACTTTGGGAGGTGAGGAGGAGGATTTGCTTGGGAGGAGGATTTGAGACAGGCTG 128042

Qy 361 GGCCAGCTAGGAGACCTTGTCTTACGCAAAACAAATTAAGTGGGCTGGTGGCGTGC 420
Db 128041 GGCCAGCTAGGAGACCTTGTCTTACGCAAAACAAATTAAGTGGGCTGGTGGCGTGC 127982

Qy 421 CCCTGTGCTCCAGCTACTCAGGAGGCTGAGGAGGAGGATTCGCTTGGTGGGAGGTT 480
Db 127981 CCCTGTGCTCCAGCTACTCAGGAGGCTGAGGAGGAGGATTCGCTTGGTGGGAGGTT 127922

Qy 481 GAGGCTGAGTAAGCTATGACACACGCTGCTGACCTCCACCTTGGGTGACAGAGTGAACC 540
Db 127921 GAGGCTGAGTAAGCTATGACACACGCTGCTGACCTCCACCTTGGGTGACAGAGTGAACC 127862

Qy 541 CTGCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 600
Db 127861 CTGCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 127803

Qy 601 GCCAGTGAAGACCCAGAGCTTATATTTAATATGCTCATTCACATAAACATCCGCA 660
Db 127802 GCCAGTGAAGACCCAGAGCTTATATTTAATATGCTCATTCACATAAACATCCGCA 127743

Qy 661 GGCCAGAGAGTGCAGGCTGTAGGAATGACCCAACTGGGAGGAGGAGGAGGAGGAGGAG 720
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Db 127682 GCCACTGGGAGCTCTGGGAGACAGAGCTGCTCCCGGGCCCTCAGGCGCTTCCCTG 127623

Qy 781 ACTCCCTGTCTTAGATGATCCAGGTGGATCCCGGAGGCGGCGCTTCGCGCCCA 840
Db 127622 ACTCCCTGTCTTAGATGATCCAGGTGGATCCCGGAGGCGGCGCTTCGCGCCCA 127563

Qy 841 GCGACGATCTCACCTCTTTGAAAAGCAGCTCCAGTTACAAAGAACTCAGCTCAATTTCC 900
Db 127562 GCGACGATCTCACCTCTTTGAAAAGCAGCTCCAGTTACAAAGAACTCAGCTCAATTTCC 127503

Qy 901 ACAAGTACTGCTCTCACTGAGGGGGCCAGGGTGGGGAGGACACACTAGGAC 960
Db 127502 ACAAGTACTGCTCTCACTGAGGGGGCCAGGGTGGGGAGGACACACTAGGAC 127443

Qy 961 TCTCACCCGACCACTACTTCCCTAAGGTGGGACAGGCGCCCGCGCGCTTGGTGC 1020
Db 127442 TCTCACCCGACCACTACTTCCCTAAGGTGGGACAGGCGCCCGCGCGCTTGGTGC 127384

Qy 1021 CTGCTGGGTGAGCACTTCCCTGCTGAGCTGAGAGTCACTGAGGAGGAGCGCTGGC 1080
Db 127383 CTGCTGGGTGAGCACTTCCCTGCTGAGCTGAGAGTCACTGAGGAGGAGCGCTGGC 127324

Qy 1081 ACTTGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 127323 ACTTGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 127264

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Qy 1261 GGCTCTCAGTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Db 127143 GGCTCTCAGTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 127085

Qy 1321 GCAGCGTGGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
Db 127084 GCAGCGTGGGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 127025

Qy 1381 CCTTGGGCTTGGGCTGCGCAAGGTTTACTCTGCCCCCACTGGCCCCCAGATCAGT 1440
Db 127024 CCTTGGGCTTGGGCTGCGCAAGGTTTACTCTGCCCCCACTGGCCCCCAGATCAGT 126965

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DEFINITION Homo sapiens mucolipin 1 (MCOLN1) gene, exons 6 and 7.
ACCESSION AF305576
VERSION AF305576.1 GI:11991202
KEYWORDS 5 of 8
SEGMENT Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 579)
AUTHORS Bargal,R., Avidan,N., Ben-Asher,E., Olender,Z., Zeigler,M.,
Frumkin,A., Raas-Rothschild,A., Glusman,G., Lancet,D. and Bach,G.
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ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 Bassi, M.T., Manzoni, M., Monti, E., Pizzo, M.T., Ballabio, A. and Borsani, G.
TITLE	Cloning of the gene encoding a novel integral membrane protein, muculipidin- and identification of the two major founder mutations causing muculipidosis type IV
JOURNAL	Am. J. Hum. Genet. 67 (5), 1110-1120 (2000)
MEDLINE	20489855 11013137
REFERENCE	2 (bases 1 to 2272)
AUTHORS	Borsani, G.
TITLE	Direct Substitution
JOURNAL	Submitted (102-AUG-2000) Borsani G., Telethon Institute of Genetics and Medicine, Via Olgettina 58, 20132 Milano, ITALY
REMARK	Revised by author
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BASE COUNT	422 a 748 c 647 g 455 t
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Query Match	29.5%; Score 442.6; DB 9; Length 2272;
Best Local Similarity	97.0%; Pred. No. 5.9e-103;
Matches 451;	Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy	795 GACTGCATCCAGGTGGATCCCCCGAGCGGCCCTCCGCCGCCCGACGAGCATCTCACC 854
Db	651 GACTGCATCCAGGTGGATCCCCCGAGCGGCCCTTCGCCCGCCAGCGACATCTCACC 710
Qy	855 CTCTTGAAGACAGCTCCAGTTACAGAACCTCAGCTCAATTCACAACTACTGCTG 914
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Qy	915 CTCACTCGAGGGGGCCCGAGGTGGGGAGGCAGCACACTAGGCACCTCTCACCCAGCAA 974
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Qy	975 CTAATTCCTTAAGTGGGACAGGGCCCCCGCCCGCTGGTGGTGGTGGGTGAGCA 1034
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Qy	1035 CTTCCCTGCCAGCTCAGAGTCACAGTGCAGTGCAGGGGACCGCTGGCACTGGGGCCGGAA 1094
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS      1 (bases 1 to 164293)
              DOE Joint Genome Institute, Stanford Human Genome Center and Los
              Alamos National Laboratory.
TITLE        Direct Submission
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 164293)
              DOE Joint Genome Institute.
AUTHORS      Direct Submission
JOURNAL      Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE    3 (bases 1 to 164293)
              DOE Joint Genome Institute.
AUTHORS      Direct Submission
JOURNAL      Submitted (06-FEB-2002) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE    4 (bases 1 to 164293)
              DOE Joint Genome Institute.
AUTHORS      Direct Submission
JOURNAL      Submitted (13-APR-2002) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE    5 (bases 1 to 164293)
              DOE Joint Genome Institute.
AUTHORS      Direct Submission
JOURNAL      Submitted (31-DEC-2002) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE    6 (bases 1 to 164293)
              DOE Joint Genome Institute, Stanford Human Genome Center and Los
              Alamos National Laboratory.
AUTHORS      Direct Submission
JOURNAL      Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
              Drive, Walnut Creek, CA 94598, USA
COMMENT      On Mar 13, 2003 this sequence version replaced gi:27436782.
              Draft Sequence Produced by DOE Joint Genome Institute
              www.jgi.doe.gov
              National Laboratory
              www-shgc.stanford.edu
              Quality: Phrap quality >=40 100% of Sequence;
              Estimated Total Number of Errors is 0.1.
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Best Local Similarity 74.6%; Pred. No. 1.6e-46;
Matches 282; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
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QY 374 GACTTGTCTTACGCAACAACAATAGTGGCGTGGTGGCGTCCCTGTGTGTCCTCA 433
Db 64235 GACCTGTCTCTACAAAAAATCAATATAGTGGGCATGTTGGTGTGCTGTGGTCCCA 64176
QY 434 GCTACTCAGGAGGCTGAGCGAGGAGGATCGCTTCACTGCTCGGAGGTTGAGCTGCAGTAA 493
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QY 494 GCTATGACACCGTGTGCTGACTCCACCTGGGTGACAGAGTGAGCCCTGTCTCAAAAA 553
Db 64115 GCTATGATCAGCACTGCTGCTCCAGCTGGGTACGAGCAACCCCTGTCTCCAAACA 64056
QY 554 AAAAAAAGAAAAAAGAAAAA 571
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LOCUS      AC022403      89666 bp      DNA      linear      HTG 29-JAN-2002
DEFINITION Homo sapiens chromosome 15 clone CTD-2120M24 map 15q21, WORKING
            DRAFT SEQUENCE, 19 ordered pieces.
ACCESSION  AC022403
VERSION     AC022403.4 GI:8199326
KEYWORDS   HTG; HTGS_PHASE2; HTGS_CANCELLED; HTGS_DRAFT.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 89666)
AUTHORS     Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,
            Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A.,
            James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T.
            and Hood, L.
TITLE       Sequencing of human chromosome 15 D15S146-D15S117 region
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 89666)
AUTHORS     Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,
            Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A.,
            James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T.
            and Hood, L.
TITLE       Direct Submission
JOURNAL      Submitted (03-FEB-2000) Multimegabase Sequencing Center, University
            of Washington, PO BOX 357730, Seattle, WA 98195, USA
COMMENT      On Jun 2, 2000 this sequence version replaced gi:7158043.
            ----- Genome Center
            Center: Multimegabase Sequencing Center
            Center code: UMMSC
            Web site: http://chroma.mbt.washington.edu/msg_www
            Contact: leorowensystemsbiology.org
            ----- Summary Statistics
            Sequencing vector: pUC18; L08752
            Chemistry: Dye-terminator Big Dye; 90% of reads
            Chemistry: Dye-primer Big Dye; 10% of reads
            Assembly program: Phrap; version 0.990399
            Insert size: 75000; agarose-fp
            Quality coverage: 3.0x in Q20 bases; sum-of-contigs
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            Sequence Quality Assessment:
            This entry has been annotated with sequence quality
            estimates computed by the Phrap assembly program.
            All manually edited bases have been reduced to quality zero.
            Quality levels above 40 are expected to have less than
            1 error in 10,000 bp.
            Base-by-base quality values are not generally visible from the
            GenBank flat file format but are available as part
            of this entry's ASN.1 file.
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 19 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submitter.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            * 1 6942: contig of 6942 bp in length
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            * 7043 14498: contig of 7456 bp in length
            * 14499 14598: gap of unknown length

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* 14599 17985: contig of 3387 bp in length
* 17986 18085: gap of unknown length
* 18086 21974: contig of 3889 bp in length
* 21975 22074: gap of unknown length
* 22075 25353: contig of 3279 bp in length
* 25354 25453: gap of unknown length
* 25454 33338: contig of 7885 bp in length
* 33339 33438: gap of unknown length
* 33439 35089: contig of 1651 bp in length
* 35090 35189: gap of unknown length
* 35190 38839: contig of 3650 bp in length
* 38840 38939: gap of unknown length
* 38940 49430: contig of 10491 bp in length
* 49431 49530: gap of unknown length
* 49531 52527: contig of 2997 bp in length
* 52528 52627: gap of unknown length
* 52628 58067: contig of 5440 bp in length
* 58068 58167: gap of unknown length
* 58168 60432: contig of 2265 bp in length
* 60433 60532: gap of unknown length
* 60533 62313: contig of 1781 bp in length
* 62314 62413: gap of unknown length
* 62414 65883: contig of 3470 bp in length
* 65884 65983: gap of unknown length
* 65984 72930: contig of 6947 bp in length
* 72931 73030: gap of unknown length
* 73031 74718: contig of 1688 bp in length
* 74719 74818: gap of unknown length
* 74819 76840: contig of 2022 bp in length
* 76841 76940: gap of unknown length
* 76941 78424: contig of 1484 bp in length
* 78425 78524: gap of unknown length
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Query Match          14.9%; Score 223.6; DB 2; Length 89666;
Best Local Similarity 82.6%; Pred. No. 2.4e-46;
Matches 256; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 269 GGCTGGCAGCGTGGCTCAGCCCTATATACAGCACTTTGGGAGGCTGAGGAGGAAGGA 328
Db 23783 GGCCAGCGGTGGTGGCTCACACCTGTATATCCAGTACTTTGGGAGGCTGAGGTGGAGGT 23724

QY 329 TTGCTTGAGGCGCAGAGTTTTCAGACCACTGGCGGACCTAGGAGACCTGTCTCTACG 388
Db 23723 TCGCTTAAGCCAGAGGTTCAGACCACTGGCGGACATAGTACACCTTGTCTCTAC 23664

QY 389 CACAAAACAATTAGCTGGGCGTGGTGGCGTCCCTGTGGTCCAGCTACTCAGGAGGCT 448
Db 23663 AAAAAAAAAAATTACGAGGCGGTGGTGGGCACACACTGTAGTCCCGAGCTCTCGAGGCT 23604

QY 449 GAGCAGGAGATCGCTTGTAGTCCGGAGGTTGAGGCTGCGAGTATGACCAACGCTG 508
Db 23603 GAGTAGGAGGATTCCTTGAGCCCTGGGAGGAGAGTTTGCAAGTAAAGCGCTGTTTGTGCG 23544

QY 509 CTGCACCTCCACCTGGGTGGTACAGAGTACAGCCCTGTCTCTCAAAAAAAGAAAAA 568
Db 23543 CTGCACCTCCACCTGGGTGGTACGAGTACAGCCCTGTCTCTCAAAAAAAGAAAAA 23484

QY 569 AAACAAGTAT 578
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RESULT 10 AC069335

LOCUS AC069335 155521 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-723C11 from 7, complete sequence.

ACCESSION AC069335

VERSION AC069335.17 GI:15290496

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 155521)

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)

9063792

9847074

2 (bases 1 to 155521)

Ozersky, P., Du, H. and Maupin, R.

The sequence of Homo sapiens BAC clone RP11-723C11

Unpublished (2001)

3 (bases 1 to 155521)

Waterston, R.H.

Direct Submission

Submitted (27-MAY-2000) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

4 (bases 1 to 155521)

Waterston, R.H.

Direct Submission

Submitted (25-AUG-2001) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

5 (bases 1 to 155521)

Waterston, R.H.

Direct Submission

Submitted (26-AUG-2001) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

6 (bases 1 to 155521)

Waterston, R.

Direct Submission

Submitted (09-JAN-2002) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Aug 25, 2001 this sequence version replaced gi:13431253.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

Center project name: H_NH0723C11

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the

Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-785H2; the clone sequenced to the right is RP4-592P3, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-723C11; actual end is at base position 46589 of RP4-592P3.

Polymorphisms exist between AC069335 and AC006452.

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Query Match 14.9%; Score 223; DB 9; Length 155521;
Best Local Similarity 79.1%; Fred. NO. 3.7e-46;
Matches 265; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 243 CTGCTGGATTAAATCAACAGCTGGTGGCGACGGTGGCTCAGCCCTATATACCAG 302
Db 32084 CCGAGGAGCTGAGATGAATTGATAGCCGCCACATCTGTAGTCCCAG 32143
QY 303 CACTTTGGAGGTGAGGAGGAGGATGCTTGAGGCCAGAGTTTGAGACCCAGCTGGG 362
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Qy 483 GCCTCAGTAAGCTATGACACGCTGCTGCTCACTCCACCTGGTGCACAGAGTGACACCT 542
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AC093695 AC093695.1 GI:15487543
VERSION HTG; HTGS_PHASE1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193267)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 193267)
Waterston,R.H.
Direct Submission
Submitted (07-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0795E24

* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
* 1129: contig of 1129 bp in length
* 1130 1229: gap of unknown length
* 1230 2643: contig of 1414 bp in length
* 2644 2743: gap of unknown length
* 2744 4089: contig of 1346 bp in length
* 4090 4189: gap of unknown length
* 4190 5968: contig of 1779 bp in length
* 5969 6068: gap of unknown length
* 6069 7428: contig of 1360 bp in length
* 7429 7528: gap of unknown length
* 7529 8564: contig of 1036 bp in length
* 8565 8665: gap of unknown length
* 8666 9957: contig of 1293 bp in length
* 9958 10057: gap of unknown length
* 10058 12344: contig of 2287 bp in length
* 12345 12444: gap of unknown length
* 12445 14185: contig of 1741 bp in length
* 14186 14285: gap of unknown length
* 14286 15887: contig of 1602 bp in length
* 15888 15987: gap of unknown length

15988 18056: contig of 2069 bp in length
18057 18156: gap of unknown length
18157 19426: contig of 1270 bp in length
19427 19526: gap of unknown length
19527 21887: contig of 2361 bp in length
21888 21987: gap of unknown length
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30623 30722: gap of unknown length
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33002 33101: gap of unknown length
33102 34666: contig of 1565 bp in length
34667 34766: gap of unknown length
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50106 53138: contig of 3033 bp in length
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14.9%; Score 223; DB 2; Length 193267;

Best Local Similarity 79.1%; Pred. No. 3.8e-46;
 Matches 265; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
 Qy 243 CTGCTGGGATTAATCAACAGCTGTGGCTGGCGGCGGCTGCTACGCTATATACAG 302
 Db 4548 CCAGGAGCTGAGATGAATTTGTAAGCCCGAGCATGGTGGCCACATCTGTAGTCCAG 4607
 Qy 303 CACTTTGGGAGGCTGAGGAGGAGGATTCCTTCAGGCCCAAGATTTGAGACCACTGGG 362
 Db 4608 CATTTGGGAGGCTGAGGAGGAGGATTCCTTCAGGCCCAAGATTTGAGACCACTGGG 4667
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 Db 4668 CAACATGGCAAAATCCTGTCTCTACCAAAATCAAAATAGCTGGGCTGATGTCATGC 4727
 Qy 423 CTGTGCTCCAGCTACTCTCAGGAGGCTGAGGAGGAGGATCGCTTCAGTCCGGGAGTTCA 482
 Db 4728 CTGTAGTCTGAGCTACTCGGAGGCTGAGGAGGAGGATCACTTGAGTCTGGAGGTCAA 4787
 Qy 483 GGCTGAGTAAGTATGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 542
 Db 4788 GGCTGAGTGAAGCAAGATCATGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4847
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RESULT 12

AC084756/c

LOCUS

DEFINITION

AC084756

AC084756

AC084756

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AC084756

AC084756 166138 bp DNA linear PRI 23-JUN-2001
 Homo sapiens chromosome 15 clone RP11-120K9 map 15q21.2, complete
 sequence.

AC084756 AC027538

AC084756.3 GI:14530845

HTG.

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

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Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 166138)

Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,

Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,

Pate, D. and Hood, L.

Sequencing of human chromosome 15 D15S146-D15S117 region

Unpublished

2 (bases 1 to 166138)

Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,

Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A.,

Nesbitt, R., Traicoff, R. and Hood, L.

Direct Submission

Submitted (15-NOV-2000) Multimegabase Sequencing Center, Institute

for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA

98105, USA

3 (bases 1 to 166138)

Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,

Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R.,

Pate, D. and Hood, L.

Direct Submission

Submitted (23-JUN-2001) Multimegabase Sequencing Center, Institute

for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA

98105, USA

On Jun 23, 2001 this sequence version replaced gi:13489137.

----- Genome Center

Center: Multimegabase Sequencing Center

Web site: http://chroma.mbt.washington.edu/msg_wmw

Contact: leorowen@systemsbiology.org

Drafting center: WIBR

----- Summary Statistics

Sequencing vector: pUC18; 108752

Chemistry: Dye-terminator Big Dye; 90% of reads

Chemistry: Dye-primer Big Dye; 10% of reads

Assembly program: Phrap; version 0.990399

Note: Data from overlapping BACs AC022403 [drafting center UWMSCL], AC012170 [drafting center UWMSCL], AC012100 [drafting center UWMSCL], and AC010770 [drafting center WIBR] was added for finishing.

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Matches 253; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy 329 TTGCTTGGGCGCAGAGTTGAGACCAGCTGGGCCAGCTAGGAGAGCTTGTCTCTACG 388
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Qy 389 CACAAACAAATTAGCTGGCGTGGTGGCGTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 448
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Qy 449 GAGCAGAGAGATCGTTGATTCGGGAGGTTGAGGCTGCAGTATGACCAACCGTGTG 508
Db 30143 GAGGTAGGAGGATTCCTTGGAGCTGGGAGGAGGAGTTCAGTAAAGCGTGTGTGTCGG 30084

Qy 509 CTGCACCTCCACCTGGGTGACAGGTGAGACCTGTCTCAAAAAAAAAAAAAAAAAAAAA 568
Db 30083 CTGCACCTCCACCTGGGTGACAGGTGAGACCTGTCTCTCAAAAAAAAAAAAAAAAAAAAA 30024

Qy 569 AAACA 573
Db 30023 AAAAA 30019

RESULT 13
AC007501/c

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DEFINITION Homo sapiens chromosome 16 clone RPC1-11_67I13, complete sequence.
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VERSION    AC007501.2 GI:6806839
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 162617)
AUTHORS   Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson,D.,
            Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L.,
            Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Tatum,O.,
            Campbell,C., Fawcett,J., Maltbie,M., Bussod,M., Sutherland,R.,
            Han,C. and Deaven,L.
            Sequencing of Human Chromosome 16q12
            Unpublished
            2 (bases 1 to 162617)
AUTHORS   Ricke,D.O.
TITLE     Large Scale Sequence Analysis and Annotation with the Sequence
            Comparison Analysis (SCAN) System
JOURNAL    Unpublished
REFERENCE  3 (bases 1 to 162617)
AUTHORS   Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson,D.,
            Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L.,
            Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Tatum,O.,
            Campbell,C., Fawcett,J., Maltbie,M., Bussod,M., Sutherland,R.,
            McMurry,K., Han,C. and Deaven,L.
            Direct Submission
            Submitted (06-MAY-1999) Center for Human Genome Studies, DOE Joint
            Genome Institute, Los Alamos National Laboratory, MS M888, Los
            Alamos, NM 87545, USA
            4 (bases 1 to 162617)
AUTHORS   Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson,D.,
            Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L.,
            Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Tatum,O.,
            Campbell,C., Fawcett,J., Maltbie,M., Bussod,M., Sutherland,R.,
            McMurry,K., Han,C. and Deaven,L.
            Direct Submission
            Submitted (28-JAN-2000) Center for Human Genome Studies, DOE Joint
            Genome Institute, Los Alamos National Laboratory, MS M888, Los
            Alamos, NM 87545, USA
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DB 160154 GCCTGGCATACTGTGTTAAATATCATCTTAGCCAGGTGGTAGTTTACAACTGC 160095
QY 296 ATACACAGCACTTTGGGAGGCTGAGGAGGAGGATTGCTTGAGGCCAGAGTTTGAGACCA 355
DB 160094 ATCTGGCATTITGGGAGGCTGAGGTGGGTGGATCGCTTAGGCCAGAGTTTGAGACCA 160035
QY 356 GCCTGGCCACGTAGGAGACCTTGCTCTTAGCACA--AACAATTAAGCTGGCGCTGGT 413
DB 160034 GCCTGGCAACATAGAGAAACCTTGTCTCTACAAAAATAAAAAATTAAGCTGGCTGTGAT 159975
QY 414 GCGTSCCCCTGTGTGTCCTCCAGCTACTCAGGAGGCTGAGCAGGAGATCGTTGAGTCGG 473

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Qy	534	TGAGACCTGTCTCAAAAAAAAAAAAAAAAAAAAAAACAAGTATGCTTAGTGTGAGTGT	593
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Qy	594	GACTCTTGCCACGTAGAAAGCACCAGATGTTATATTTTAATA	635
Db	159794	CTCAGTCAGAGAAATGATTACAGATATCTTTTCATTTAAAA	159753

[illegible]

BASE COUNT	53956 a	33815 c	31727 g	49704 t	ORIGIN
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Qy	296	ATACCAAGCACTTTGGGAGGCTGAGGAGGAAGGATTGCTTGAGGCCAGAAAGTTTGAGACCA	355		
Db	108780	ATCTTGGCAITTTGGGAGGCTGAGTGGTGGATCGCTTGAGCCAGAAAGTTTGAGACCA	108721		
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LOCUS	Homo sapiens chromosome 11 clone CTD-202104 map 11, LOW-PASS				
DEFINITION	SEQUENCE SAMPLING.				
ACCESSION	AC133460				
VERSION	AC133460.1 GI:22795351				
KEYWORDS	HTG; HTGS_PHRASE0.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 59634)				
TITLE	Birren, B., Nusbaum, C. and Lander, E.				
JOURNAL	Homo sapiens chromosome 11, clone CTD-202104				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 59634)				
TITLE	Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, V., Collimore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gorg, S., Graham, L., Grand-Pierre, N., Hagos, B., Hariton, L., Hulme, W., Iliev, I., Johnson, P., Jones, C., Kamat, A.				

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RN/RepeatMasker.html>

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L28118
 Center clone name: 2021_O_4

* NOTE: This record contains 74 individual
 sequencing reads that have not been assembled into
 contigs. Runs of N are used to separate the reads
 and the order in which they appear is completely
 arbitrary. Low-pass sequence sampling is useful for
 identifying clones that may be gene-rich and allows
 overlap relationships among clones to be deduced.
 However, it should not be assumed that this clone
 will be sequenced to completion. In the event that
 the record is updated, the accession number will
 be preserved.

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 3733 3832: gap of 100 bp
 3833 4544: contig of 712 bp in length
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 4645 5323: contig of 679 bp in length
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